

30/175

Pro Phe Lys Cys Thr Tyr Cys Ser Arg Leu Phe Lys His Lys Arg Ser
 145 150 155 160
 Arg Asp Arg His Ile Lys Leu His Thr Gly Asp Lys Lys Tyr His Cys
 165 170 175
 Ser Glu Cys Asp Ala Ala Phe Ser Arg Ser Asp His Leu Lys Ile His
 180 185 190
 Leu Lys Thr His Thr Ser Asn Lys Pro Tyr Lys Cys Ala Ile Cys Arg
 195 200 205
 Arg Gly Phe Leu Ser Ser Ser Ser Leu His Gly His Met Gln Val His
 210 215 220
 Glu Arg Asn Lys Asp Gly Ser Gln Ser Gly Ser Arg Met Glu Asp Trp
 225 230 235 240
 Lys Met Lys Asp Thr Gln Lys Cys Ser Gln Cys Glu Glu Gly Phe Asp
 245 250 255
 Phe Pro Glu Asp Leu Gln Lys His Ile Ala Glu Cys His Pro Glu Cys
 260 265 270
 Ser Pro Asn Glu Asp Arg Ala Ala Leu Gln Cys Val Tyr Cys His Glu
 275 280 285
 Leu Phe Val Glu Glu Thr Ser Leu Met Asn His Met Glu Gln Val His
 290 295 300
 Ser Gly Glu Lys Lys Asn Ser Cys Ser Ile Cys Ser Glu Ser Phe His
 305 310 315 320
 Thr Val Glu Glu Leu Tyr Ser His Met Asp Ser His Gln Gln Pro Glu
 325 330 335
 Ser Cys Asn His Ser Asn Ser Pro Ser Leu Val Thr Val Gly Tyr Thr
 340 345 350
 Ser Val Ser Ser Thr Thr Pro Asp Ser Asn Leu Ser Val Asp Ser Ser
 355 360 365
 Thr Met Val Glu Ala Ala Pro Pro Ile Pro Lys Ser Arg Gly Arg Lys
 370 375 380
 Arg Ala Ala Gln Gln Thr Pro Asp Met Thr Gly Pro Ser Ser Lys Gln
 385 390 395 400
 Ala Lys Val Thr Tyr Ser Cys Ile Tyr Cys Asn Lys Gln Leu Phe Ser
 405 410 415
 Ser Leu Ala Val Leu Gln Ile His Leu Lys Thr Met His Leu Asp Lys
 420 425 430
 Pro Glu Gln Ala His Ile Cys Gln Tyr Cys Leu Glu Val Leu Pro Ser
 435 440 445
 Leu Tyr Asn Leu Asn Glu His Leu Lys Gln Val His Glu Ala Gln Asp
 450 455 460
 Pro Gly Leu Ile Val Ser Ala Met Pro Ala Ile Val Tyr Gln Cys Asn
 465 470 475 480
 Phe Cys Ser Glu Val Val Asn Asp Leu Asn Thr Leu Gln Glu His Ile
 485 490 495
 Arg Cys Ser His Gly Phe Ala Asn Pro Ala Ala Lys Asp Ser Asn Ala
 500 505 510
 Phe Phe Cys Pro His Cys Tyr Met Gly Phe Leu Thr Asp Ser Ser Leu
 515 520 525

31/175

Glu Glu His Ile Arg Gln Val His Cys Asp Leu Ser Gly Ser Arg Phe
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 Gly Ser Pro Val Leu Gly Thr Pro Lys Glu Pro Val Val Glu Val Tyr
 545 550 555 560
 Ser Cys Ser Tyr Cys Thr Asn Ser Pro Ile Phe Asn Ser Val Leu Lys
 565 570 575
 Leu Asn Lys His Ile Lys Glu Asn His Lys Asn Ile Pro Leu Ala Leu
 580 585 590
 Asn Tyr Ile His Asn Gly Lys Lys Ser Arg Ala Leu Ser Pro Leu Ser
 595 600 605
 Pro Val Ala Ile Glu Gln Thr Ser Leu Lys Met Met Gln Ala Val Gly
 610 615 620
 Gly Ala Pro Ala Arg Pro Thr Gly Glu Tyr Ile Cys Asn Gln Cys Gly
 625 630 635 640
 Ala Lys Tyr Thr Ser Leu Asp Ser Phe Gln Thr His Leu Lys Thr His
 645 650 655
 Leu Asp Thr Val Leu Pro Lys Leu Thr Cys Pro Gln Cys Asn Lys Glu
 660 665 670
 Phe Pro Asn Gln Glu Ser Leu Leu Lys His Val Thr Ile His Phe Met
 675 680 685
 Ile Thr Ser Thr Tyr Tyr Ile Cys Glu Ser Cys Asp Lys Gln Phe Thr
 690 695 700
 Ser Val Asp Asp Leu Gln Lys His Leu Leu Asp Met His Thr Phe Val
 705 710 715 720
 Phe Phe Arg Cys Thr Leu Cys Gln Glu Val Phe Asp Ser Lys Val Ser
 725 730 735
 Ile Gln Leu His Leu Ala Val Lys His Ser Asn Glu Lys Lys Val Tyr
 740 745 750
 Arg Cys Thr Ser Cys Asn Trp Asp Phe Arg Asn Glu Thr Asp Leu Gln
 755 760 765
 Leu His Val Lys His Asn His Leu Glu Asn Gln Gly Lys Val His Lys
 770 775 780
 Cys Ile Phe Cys Gly Glu Ser Phe Gly Thr Glu Val Glu Leu Gln Cys
 785 790 795 800
 His Ile Thr Thr His Ser Lys Lys Tyr Asn Cys Lys Phe Cys Ser Lys
 805 810 815
 Ala Phe His Ala Ile Ile Leu Leu Glu Lys His Leu Arg Glu Lys His
 820 825 830
 Cys Val Phe Glu Thr Lys Thr Pro Asn Cys Gly Thr Asn Gly Ala Ser
 835 840 845
 Glu Gln Val Gln Lys Glu Glu Val Glu Leu Gln Thr Leu Leu Thr Asn
 850 855 860
 Ser Gln Glu Ser His Asn Ser His Asp Gly Ser Glu Glu Asp Val Asp
 865 870 875 880
 Thr Ser Glu Pro Met Tyr Gly Cys Asp Ile Cys Gly Ala Ala Tyr Thr
 885 890 895
 Met Glu Thr Leu Leu Gln Asn His Gln Leu Arg Asp His Asn Ile Arg
 900 905 910

32/175

Pro Gly Glu Ser Ala Ile Val Lys Lys Lys Ala Glu Leu Ile Lys Gly
 915 920 925
 Asn Tyr Lys Cys Asn Val Cys Ser Arg Thr Phe Phe Ser Glu Asn Gly
 930 935 940
 Leu Arg Glu His Met Gln Thr His Leu Gly Pro Val Lys His Tyr Met
 945 950 955 960
 Cys Pro Ile Cys Gly Glu Arg Phe Pro Ser Leu Leu Thr Leu Thr Glu
 965 970 975
 His Lys Val Thr His Ser Lys Ser Leu Asp Thr Gly Asn Cys Arg Ile
 980 985 990
 Cys Lys Met Pro Leu Gln Ser Glu Glu Glu Phe Leu Glu His Cys Gln
 995 1000 1005
 Met His Pro Asp Leu Arg Asn Ser Leu Thr Gly Phe Arg Cys Val Val
 1010 1015 1020
 Cys Met Gln Thr Val Thr Ser Thr Leu Glu Leu Lys Ile His Gly Thr
 1025 1030 1035 1040
 Phe His Met Gln Lys Thr Gly Asn Gly Ser Ala Val Gln Thr Thr Gly
 1045 1050 1055
 Arg Gly Gln His Val Gln Lys Leu Tyr Lys Cys Ala Ser Cys Leu Lys
 1060 1065 1070
 Glu Phe Arg Ser Lys Gln Asp Leu Val Lys Leu Asp Ile Asn Gly Leu
 1075 1080 1085
 Pro Tyr Gly Leu Cys Ala Gly Cys Val Asn Leu Ser Lys Ser Ala Ser
 1090 1095 1100
 Pro Gly Ile Asn Val Pro Pro Gly Thr Asn Arg Pro Gly Leu Gly Gln
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 Asn Glu Asn Leu Ser Ala Ile Glu Gly Lys Gly Lys Val Gly Gly Leu
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 Lys Thr Arg Cys Ser Ser Cys Asn Val Lys Phe Glu Ser Glu Ser Glu
 1140 1145 1150
 Leu Gln Asn His Ile Gln Thr Ile His Arg Glu Leu Val Pro Asp Ser
 1155 1160 1165
 Asn Ser Thr Gln Leu Lys Thr Pro Gln Val Ser Pro Met Pro Arg Ile
 1170 1175 1180
 Ser Pro Ser Gln Ser Asp Glu Lys Lys Thr Tyr Gln Cys Ile Lys Cys
 1185 1190 1195 1200
 Gln Met Val Phe Tyr Asn Glu Trp Asp Ile Gln Val His Val Ala Asn
 1205 1210 1215
 His Met Ile Asp Glu Gly Leu Asn His Glu Cys Lys Leu Cys Ser Gln
 1220 1225 1230
 Thr Phe Asp Ser Pro Ala Lys Leu Gln Cys His Leu Ile Glu His Ser
 1235 1240 1245
 Phe Glu Gly Met Gly Gly Thr Phe Lys Cys Pro Val Cys Phe Thr Val
 1250 1255 1260
 Phe Val Gln Ala Asn Lys Leu Gln Gln His Ile Phe Ser Ala His Gly
 1265 1270 1275 1280
 Gln Glu Asp Lys Ile Tyr Asp Cys Thr Gln Cys Pr Gln Lys Phe Phe
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33/175

Phe Gln Thr Glu Leu Gln Asn His Thr Met Thr Gln His Ser Ser
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<210> 28
 <211> 1988
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (160).. (876)

<400> 28

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ccaggaagtt cagagagaac agaatttaag aagtgcaca tggccagggg ctgcctctgc 180
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accgagaaca acgtggggct gaagaacgcc tggaaacatca tccaggctga gatgcgatgc 600
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cgctgctgca tggagaactc ccagggtgc gggcgcaacg ccaccacgcc tttgtggaga 720
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34/175

<210> 29
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 29
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 Trp Leu Ser Val Ser Gln Gly Asn Phe Ala Thr Phe Ser Pro Ser Phe
 35 40 45
 Pro Ser Leu Ser Ala Ala Asn Leu Val Ile Ala Ile Gly Thr Ile Val
 50 55 60
 Met Val Thr Gly Phe Leu Gly Cys Leu Gly Ala Ile Lys Glu Asn Lys
 65 70 75 80
 Cys Leu Leu Leu Ser Phe Phe Ile Val Leu Leu Val Ile Leu Leu Ala
 85 90 95
 Glu Leu Ile Leu Leu Ile Leu Phe Phe Val Tyr Met Asp Lys Val Asn
 100 105 110
 Glu Asn Ala Lys Lys Asp Leu Lys Glu Gly Leu Leu Leu Tyr His Thr
 115 120 125
 Glu Asn Asn Val Gly Leu Lys Asn Ala Trp Asn Ile Ile Gln Ala Glu
 130 135 140
 Met Arg Cys Cys Gly Val Thr Asp Tyr Thr Asp Trp Tyr Pro Val Leu
 145 150 155 160
 Gly Glu Asn Thr Val Pro Asp Arg Cys Cys Met Glu Asn Ser Gln Gly
 165 170 175
 Cys Gly Arg Asn Ala Thr Thr Pro Leu Trp Arg Thr Gly Cys Tyr Glu
 180 185 190
 Lys Val Lys Met Trp Phe Asp Asp Asn Lys His Val Leu Gly Thr Val
 195 200 205
 Gly Met Cys Ile Leu Ile Met Gln Ile Leu Gly Met Ala Phe Ser Met
 210 215 220
 Thr Leu Phe Gln His Ile His Arg Thr Gly Lys Lys Tyr Asp Ala
 225 230 235

<210> 30
 <211> 1900
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (128).. (1195)

35/175

<400> 30

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ccagtccatg ggttcttatg gacctttcgg caggatgccc acatacagtc agttcagttc 180
gagttcctta gttgggcagc agtttggtgc tgttggtgtt gctggaagct ctttgacatc 240
ctttggaaca gaaacatcaa acagtgggtac cttaccccaa agtagtgogg ttggttctgc 300
ctttacacag gatacaagat ctctaaaaac acagttatct caaggtcgtc caagccctca 360
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cttacctgct ccagcagctg ttgggagaag gagtctgtga tcaaccaggc ctttgccatc 480
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aaggccagaa aatgagcaac tcagaaatga taacaagaga caagtagctc cagggtgctc 600
ttcagctcca aggagagggc gtgggggtca togggggtggc aggggaagat ttggtattcg 660
gcgagatggg ccaatgaaat ttgagaaaga ctttgacttt gaaagtgcaa atgcacaatt 720
caacaaggaa gagattgaca gagagtttca taataaaact aaattaaaag aagataaact 780
tgagaaacag gagaagcctg taaatggtga agataaagga gactcaggag ttgataccca 840
aaacagtgaa ggaaatgccg atgaagaaga tccacttgga cctaattgct attatgacaa 900
aactaaatcc ttctttgata atatttcttg tgatgacaat agagaacgga gaccaacctg 960
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tgtgtgtgtg tgtgtgtgtg tgtgtgtgtc tttttcctcc tttcttttgg ggaatcctgt 1680
aatatgaggt agcttatttc gtcaattaat taggggtgct gatggtagag aattttgtca 1740
gtcaactatg tacacacagt aaatactgtt tcttaggcaa aggtaacttt tttatatagt 1800
tgtaaaatto catttatatt cattgccaaa gaaacattaa gaactttgta tagctgtata 1860
aaaagcaact aattttttta agaataaaca ttttaaagtc 1900

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<210> 31

<211> 356

<212> PRT

<213> Homo sapiens

<400> 31

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Ser Pro Ser Ser Leu Val Gly Gln Gln Phe Gly Ala Val Gly Val Ala
          20           25           30
Gly Ser Ser Leu Thr Ser Phe Gly Thr Glu Thr Ser Asn Ser Gly Thr
          35           40           45

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36/175

Leu Pro Gln Ser Ser Ala Val Gly Ser Ala Phe Thr Gln Asp Thr Arg
 50 55 60
 Ser Leu Lys Thr Gln Leu Ser Gln Gly Arg Ser Ser Pro Gln Leu Asp
 65 70 75 80
 Pro Leu Arg Lys Ser Pro Thr Met Glu Gln Ala Val Gln Thr Ala Ser
 85 90 95
 Ala His Leu Pro Ala Pro Ala Ala Val Gly Arg Arg Ser Pro Val Ser
 100 105 110
 Thr Arg Pro Leu Pro Ser Ala Ser Gln Lys Ala Gly Glu Asn Gln Glu
 115 120 125
 His Arg Arg Ala Glu Val His Lys Val Ser Arg Pro Glu Asn Glu Gln
 130 135 140
 Leu Arg Asn Asp Asn Lys Arg Gln Val Ala Pro Gly Ala Pro Ser Ala
 145 150 155 160
 Pro Arg Arg Gly Arg Gly Gly His Arg Gly Gly Arg Gly Arg Phe Gly
 165 170 175
 Ile Arg Arg Asp Gly Pro Met Lys Phe Glu Lys Asp Phe Asp Phe Glu
 180 185 190
 Ser Ala Asn Ala Gln Phe Asn Lys Glu Glu Ile Asp Arg Glu Phe His
 195 200 205
 Asn Lys Leu Lys Leu Lys Glu Asp Lys Leu Glu Lys Gln Glu Lys Pro
 210 215 220
 Val Asn Gly Glu Asp Lys Gly Asp Ser Gly Val Asp Thr Gln Asn Ser
 225 230 235 240
 Glu Gly Asn Ala Asp Glu Glu Asp Pro Leu Gly Pro Asn Cys Tyr Tyr
 245 250 255
 Asp Lys Thr Lys Ser Phe Phe Asp Asn Ile Ser Cys Asp Asp Asn Arg
 260 265 270
 Glu Arg Arg Pro Thr Trp Ala Glu Glu Arg Arg Leu Asn Ala Glu Thr
 275 280 285
 Phe Gly Ile Pro Leu Arg Pro Asn Arg Gly Arg Gly Gly Tyr Arg Gly
 290 295 300
 Arg Gly Gly Leu Gly Phe Arg Gly Gly Arg Gly Arg Gly Gly Arg
 305 310 315 320
 Gly Gly Thr Phe Thr Ala Pro Arg Gly Phe Arg Gly Gly Phe Arg Gly
 325 330 335
 Gly Arg Gly Gly Arg Glu Phe Ala Asp Phe Glu Tyr Arg Lys Asp Asn
 340 345 350
 Lys Val Ala Ala
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<210> 32

<211> 1877

<212> DNA

<213> Homo sapiens

<220>

37/175

<221> CDS

<222> (127).. (840)

<400> 32

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<210> 33

<211> 238

<212> PRT

<213> Homo sapiens

<400> 33

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Tyr Leu Ser Arg Ala Lys Leu Lys Ala Ser Ser Arg Thr Ser Ala Leu
          20          25          30

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38/175

Leu Ser Gly Phe Ala Met Val Ala Met Val Glu Val Gln Leu Asp Ala
 35 40 45
 Asp His Asp Tyr Pro Pro Gly Leu Leu Ile Ala Phe Ser Ala Cys Thr
 50 55 60
 Thr Val Leu Val Ala Val His Leu Phe Ala Leu Met Ile Ser Thr Cys
 65 70 75 80
 Ile Leu Pro Asn Ile Glu Ala Val Ser Asn Val His Asn Leu Asn Ser
 85 90 95
 Val Lys Glu Ser Pro His Glu Arg Met His Arg His Ile Glu Leu Ala
 100 105 110
 Trp Ala Phe Ser Thr Val Ile Gly Thr Leu Leu Phe Leu Ala Glu Val
 115 120 125
 Val Leu Leu Cys Trp Val Lys Phe Leu Pro Leu Lys Lys Gln Pro Gly
 130 135 140
 Gln Pro Arg Pro Thr Ser Lys Pro Pro Ala Gly Gly Ala Ala Ala Asn
 145 150 155 160
 Val Ser Thr Ser Gly Ile Thr Pro Gly Gln Ala Ala Ala Ile Ala Ser
 165 170 175
 Thr Thr Ile Met Val Pro Phe Gly Leu Ile Phe Ile Val Phe Ala Phe
 180 185 190
 His Phe Tyr Arg Ser Leu Val Ser His Lys Thr Asp Arg Gln Phe Gln
 195 200 205
 Glu Leu Asn Glu Leu Ala Glu Phe Ala Arg Leu Gln Asp Gln Leu Asp
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 His Arg Gly Asp His Pro Leu Thr Pro Gly Ser His Tyr Ala
 225 230 235

<210> 34

<211> 2598

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (24).. (1064)

<400> 34

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 aggtcctgga ggtctcgtgg ctacacggcc tgaaagctct ggggcatctg gacctgtctg 540
 ggaaccgcct ccggaaactg cccccggggc tgctggccaa cttcaccctc ctgcgcaccc 600

7.

8.

39/175

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aattagaacg gctacatcta gaaggcaaca aattgcaagt actgggaaaa gatctcctct 720
tgccgcagcc ggacctgcgc tacctcttcc tgaacggcaa caagctggcc aggggtggcag 780
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<210> 35

<211> 347

<212> PRT

<213> Homo sapiens

<400> 35

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      20             25             30
Ala Trp Gly Val Thr Leu Ser Pro Lys Asp Cys Gln Val Phe Arg Ser
      35             40             45

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40/175

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Asp His Gly Ser Ser Ile Ser Cys Gln Pro Pro Ala Glu Ile Pro Gly
 50          55          60
Tyr Leu Pro Ala Asp Thr Val His Leu Ala Val Glu Phe Phe Asn Leu
 65          70          75          80
Thr His Leu Pro Ala Asn Leu Leu Gln Gly Ala Ser Lys Leu Gln Glu
          85          90          95
Leu His Leu Ser Ser Asn Gly Leu Glu Ser Leu Ser Pro Glu Phe Leu
          100          105          110
Arg Pro Val Pro Gln Leu Arg Val Leu Asp Leu Thr Arg Asn Ala Leu
          115          120          125
Thr Gly Leu Pro Ser Gly Leu Phe Gln Ala Ser Ala Thr Leu Asp Thr
          130          135          140
Leu Val Leu Lys Glu Asn Gln Leu Glu Val Leu Glu Val Ser Trp Leu
          145          150          155          160
His Gly Leu Lys Ala Leu Gly His Leu Asp Leu Ser Gly Asn Arg Leu
          165          170          175
Arg Lys Leu Pro Pro Gly Leu Leu Ala Asn Phe Thr Leu Leu Arg Thr
          180          185          190
Leu Asp Leu Gly Glu Asn Gln Leu Glu Thr Leu Pro Pro Asp Leu Leu
          195          200          205
Arg Gly Pro Leu Gln Leu Glu Arg Leu His Leu Glu Gly Asn Lys Leu
          210          215          220
Gln Val Leu Gly Lys Asp Leu Leu Leu Pro Gln Pro Asp Leu Arg Tyr
          225          230          235          240
Leu Phe Leu Asn Gly Asn Lys Leu Ala Arg Val Ala Ala Gly Ala Phe
          245          250          255
Gln Gly Leu Arg Gln Leu Asp Met Leu Asp Leu Ser Asn Asn Ser Leu
          260          265          270
Ala Ser Val Pro Glu Gly Leu Trp Ala Ser Leu Gly Gln Pro Asn Trp
          275          280          285
Asp Met Arg Asp Gly Phe Asp Ile Ser Gly Asn Pro Trp Ile Cys Asp
          290          295          300
Gln Asn Leu Ser Asp Leu Tyr Arg Trp Leu Gln Ala Gln Lys Asp Lys
          305          310          315          320
Met Phe Ser Gln Asn Asp Thr Arg Cys Ala Gly Pro Glu Ala Val Lys
          325          330          335
Gly Gln Thr Leu Leu Ala Val Ala Lys Ser Gln
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<210> 36

<211> 3087

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (216).. (1283)



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•

41/175

<400> 36

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42/175

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<210> 37

<211> 356

<212> PRT

<213> Homo sapiens

<400> 37

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          20           25           30
Asp Phe Arg His Thr Met His Val Gly Arg Ala Gly Asp Ala Phe Gly
          35           40           45
Asp Thr Ser Phe Leu Asn Ser Lys Ala Gly Glu Pro Asp Gly Glu Ser
          50           55           60
Leu Asp Glu Gln Pro Ser Ser Ser Ser Ser Lys Arg Ser Leu Leu Ser
          65           70           75           80
Arg Lys Phe Arg Gly Ser Lys Arg Ser Gln Ser Val Thr Arg Gly Glu
          85           90           95
Arg Glu Gln Arg Asp Met Leu Gly Ser Leu Arg Asp Ser Ala Leu Phe
          100          105          110
Val Lys Asn Ala Met Ser Leu Pro Gln Leu Asn Glu Lys Glu Ala Ala
          115          120          125
Glu Lys Gly Thr Ser Lys Leu Pro Lys Ser Leu Ser Ser Ser Pro Val
          130          135          140
Lys Lys Ala Asn Asp Gly Glu Gly Gly Asp Glu Glu Ala Gly Thr Glu
          145          150          155          160
Glu Ala Val Pro Arg Arg Asn Gly Ala Ala Gly Pro His Ser Pro Asp
          165          170          175
Pro Leu Leu Asp Glu Gln Ala Phe Gly Asp Leu Thr Asp Leu Pro Val
          180          185          190
Val Pro Lys Ala Thr Tyr Gly Leu Lys His Ala Glu Ser Ile Met Ser
          195          200          205
Phe His Ile Asp Leu Gly Pro Ser Met Leu Gly Asp Val Leu Ser Ile
          210          215          220
Met Asp Lys Glu Glu Trp Asp Pro Glu Glu Gly Glu Gly Gly Tyr His
          225          230          235          240
Gly Asp Glu Gly Ala Ala Gly Thr Il Thr Gln Ala Pro Pro Tyr Ala
          245          250          255
Val Ala Ala Pro Pro Leu Ala Arg Gln Glu Gly Lys Ala Gly Pro Asp
          260          265          270

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43/175

Leu Pro Ser Leu Pro Ser His Ala Leu Glu Asp Glu Gly Trp Ala Ala
 275 280 285
 Ala Ala Pro Ser Pro Gly Ser Ala Arg Ser Met Gly Ser His Thr Thr
 290 295 300
 Arg Asp Ser Ser Ser Leu Ser Ser Cys Thr Ser Gly Ile Leu Glu Glu
 305 310 315 320
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 325 330 335
 Arg Gln Pro Asp Lys Glu Phe Ser Phe Met Asp Glu Glu Glu Glu Asp
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<210> 38
 <211> 3305
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (41).. (586)

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44/175

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<210> 39

<211> 182

<212> PRT

<213> Homo sapiens

<400> 39

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Ala Ser Gly Asn Lys Val Ser Arg Gln Ser Val Leu Cys Gly Ser Gln
      20             25             30
Asn Ile Val Leu Asn Gly Lys Thr Ile Val Met Asn Asp Cys Ile Ile
      35             40             45
Arg Gly Asp Leu Ala Asn Val Arg Val Gly Arg His Cys Val Val Lys
      50             55             60

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45/175

Ser Arg Ser Val Ile Arg Pro Pro Phe Lys Lys Phe Ser Lys Gly Val
 65 70 75 80
 Ala Phe Phe Pro Leu His Ile Gly Asp His Val Phe Ile Glu Glu Asp
 85 90 95
 Cys Val Val Asn Ala Ala Gln Ile Gly Ser Tyr Val His Val Gly Lys
 100 105 110
 Asn Cys Val Ile Gly Arg Arg Cys Val Leu Lys Asp Cys Cys Lys Ile
 115 120 125
 Leu Asp Asn Thr Val Leu Pro Pro Glu Thr Val Val Pro Pro Phe Thr
 130 135 140
 Val Phe Ser Gly Cys Pro Gly Leu Phe Ser Gly Glu Leu Pro Glu Cys
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 Leu Pro Leu Thr Gln Val
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<210> 40

<211> 2252

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (451).. (1269)

<400> 40

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46/175

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<210> 41

<211> 273

<212> PRT

<213> Homo sapiens

<400> 41

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      20             25             30
Leu Leu Leu Leu Leu Leu Val Tyr Leu Thr Gln Pro Gly Asn Gly
      35             40             45
Asn Glu Gly Ser Val Thr Gly Ser Cys Tyr Cys Gly Lys Arg Ile Ser
      50             55             60
Ser Asp Ser Pro Pro Ser Val Gln Phe Met Asn Arg Leu Arg Lys His
      65             70             75             80
Leu Arg Ala Tyr His Arg Cys Leu Tyr Tyr Thr Arg Phe Gln Leu Leu
      85             90             95
Ser Trp Ser Val Cys Gly Gly Asn Lys Asp Pro Trp Val Gln Glu Leu
      100            105            110
Met Ser Cys Leu Asp Leu Lys Glu Cys Gly His Ala Tyr Ser Gly Ile
      115            120            125
Val Ala His Gln Lys His Leu Leu Pro Thr Ser Pro Pro Ile Ser Gln
      130            135            140
Ala Ser Glu Gly Ala Ser Ser Asp Ile Leu Thr Pro Ala Gln Met Leu
      145            150            155            160
Leu Ser Thr Leu Gln S r Thr Gln Arg Pro Thr Leu Pro Val Gly Ser
      165            170            175

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47/175

Leu Ser Ser Asp Lys Glu Leu Thr Arg Pro Asn Glu Thr Thr Ile His
 180 185 190
 Thr Ala Gly His Ser Leu Ala Ala Gly Pro Glu Ala Gly Glu Asn Gln
 195 200 205
 Lys Gln Pro Glu Lys Asn Ala Gly Pro Thr Ala Arg Thr Ser Ala Thr
 210 215 220
 Val Pro Val Leu Cys Leu Leu Ala Ile Ile Phe Ile Leu Thr Ala Ala
 225 230 235 240
 Leu Ser Tyr Val Leu Cys Lys Arg Arg Arg Gly Gln Ser Pro Gln Ser
 245 250 255
 Ser Pro Asp Leu Pro Val His Tyr Ile Pro Val Ala Pro Asp Ser Asn
 260 265 270
 Thr

<210> 42

<211> 3119

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (94).. (1212)

<400> 42

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 ggagctctgc acgtggtgat tgtgggtggg ggctttggcg ggatcgagc agccagccag 180
 ctgcaggccc tgaacgtccc ctccatgctg gtggacatga aggactcctt ccaccacaat 240
 gtggctgctc tccgagcctc cgtggagaca gggttcgcca aaaagacatt catttcttac 300
 tcggtgactt tcaaggacaa cttccggcag gggctagtag tggggataga cctgaagaac 360
 cagatggtgc tgctgcaggg tggcgaggcc ctgcccttct ctcatcttat cctggccacg 420
 ggcagcactg ggcccttccc gggcaagttt aatgagggtt ccagccagca ggccgctatc 480
 caggcctatg aggacatggt gaggcaggct cagcgctcac ggttcatcgt ggtggtggga 540
 ggaggctcgg ctggagtgga gatggcagca gagattaaaa cagaatatcc tgagaaagag 600
 gtcactctca ttactccca agtggccctg gctgacaagg agctcctgcc ctccgtccgg 660
 caggaagtga aggagatcct cctccggaag ggcgtgcagc tgctgctgag tgagcgggtg 720
 agcaatctgg aggagctgcc totcaatgag tatcgagagt acatcaaagt gcagacggac 780
 aaaggcacag aggtggccac caacctggtg attctctgca ccggcatcaa gatcaacagc 840
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 gagcacctcc aggtggaggg ccacagcaac gtctacgcca ttggtgactg tgccgacgtg 960
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48/175

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cagcccttcc tctgcacctg cctcctctgg gatgtgcatg tgttgttatg tgccttgtgt 1560
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tgggactaca ggcacgtgcc accatgcctg gctaattttt gtatttttta aatagagacg 2040
gggtttcact gtgttggcca ggctggctct gaacacctga cctcaggtga tccattcgtc 2100
ttggcctctc gaagtgtctg gattccaggc gtgagccact gcggccagca catttccact 2160
tttagatcct actccatacc acaggtttca ttttaagaaga aagagctaga taaatgtgct 2220
cttctggtta cccaccctg acagagtga tttttacacg gctagcaggg gttgagactg 2280
cagcctggcc tgccagccat tggagggtt taaggaaggg cagataatgt gactctttgc 2340
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cccagtgtgt gagcgacagg ccttcttcta ttgaattaca atattctaga aggacctacg 3060
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<210> 43

<211> 373

<212> PRT

<213> Homo sapiens

<400> 43

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Met Gly Ser Gln Val Ser Val Glu Ser Gly Ala Leu His Val Val Ile
 1             5             10             15
Val Gly Gly Gly Phe Gly Gly Ile Ala Ala Ala Ser Gln Leu Gln Ala
      20             25             30
Leu Asn Val Pro Phe Met Leu Val Asp Met Lys Asp Ser Phe His His
      35             40             45
Asn Val Ala Ala Leu Arg Ala Ser Val Glu Thr Gly Phe Ala Lys Lys
      50             55             60
Thr Phe Ile Ser Tyr Ser Val Thr Phe Lys Asp Asn Phe Arg Gln Gly
      65             70             75             80

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49/175

Leu Val Val Gly Ile Asp Leu Lys Asn Gln Met Val Leu Leu Gln Gly
 85 90 95
 Gly Glu Ala Leu Pro Phe Ser His Leu Ile Leu Ala Thr Gly Ser Thr
 100 105 110
 Gly Pro Phe Pro Gly Lys Phe Asn Glu Val Ser Ser Gln Gln Ala Ala
 115 120 125
 Ile Gln Ala Tyr Glu Asp Met Val Arg Gln Val Gln Arg Ser Arg Phe
 130 135 140
 Ile Val Val Val Gly Gly Gly Ser Ala Gly Val Glu Met Ala Ala Glu
 145 150 155 160
 Ile Lys Thr Glu Tyr Pro Glu Lys Glu Val Thr Leu Ile His Ser Gln
 165 170 175
 Val Ala Leu Ala Asp Lys Glu Leu Leu Pro Ser Val Arg Gln Glu Val
 180 185 190
 Lys Glu Ile Leu Leu Arg Lys Gly Val Gln Leu Leu Leu Ser Glu Arg
 195 200 205
 Val Ser Asn Leu Glu Glu Leu Pro Leu Asn Glu Tyr Arg Glu Tyr Ile
 210 215 220
 Lys Val Gln Thr Asp Lys Gly Thr Glu Val Ala Thr Asn Leu Val Ile
 225 230 235 240
 Leu Cys Thr Gly Ile Lys Ile Asn Ser Ser Ala Tyr Arg Lys Ala Phe
 245 250 255
 Glu Ser Arg Leu Ala Ser Ser Gly Ala Leu Arg Val Asn Glu His Leu
 260 265 270
 Gln Val Glu Gly His Ser Asn Val Tyr Ala Ile Gly Asp Cys Ala Asp
 275 280 285
 Val Arg Thr Pro Lys Met Ala Tyr Leu Ala Gly Leu His Ala Asn Ile
 290 295 300
 Ala Val Ala Asn Ile Val Asn Ser Val Lys Gln Arg Pro Leu Gln Ala
 305 310 315 320
 Tyr Lys Pro Gly Ala Leu Thr Phe Leu Leu Ser Met Gly Arg Asn Asp
 325 330 335
 Gly Val Gly Gln Ile Ser Gly Phe Tyr Val Gly Arg Leu Met Val Arg
 340 345 350
 Leu Thr Lys Ser Arg Asp Leu Phe Val Ser Thr Ser Trp Lys Thr Met
 355 360 365
 Arg Gln Ser Pro Pro
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<210> 44

<211> 3111

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (39).. (2762)

50/175

<400> 44

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gacgtgcagc tgcgaagtgc ttggatgccg tagttagcac aaggcatgaa atgcttccag 180
aattctacaa gaccgtctct cctgcactaa tatccagatt taaagagcgt gaagagaatg 240
taaaggcaga tgtttttcac gcataccttt ctcttttgaa gcaaactcgt cctgtacaaa 300
gttggctatg tgaccctgat gcaatggagc agggagaaac acctttaaca atgcttcaga 360
gtcaggttcc caacattgtt aaagctcttc acaaacagat gaaagaaaaa agtgtgaaga 420
cccgacagtg ttgttttaac atattaactg agctggtaaa tgtattacct ggggcccata 480
ctcaacacat tctgtactt gtaccaggaa tcattttctc actgaatgat aaatcaagct 540
catcgaattt gaagatcgat gctttgtcat gtctatacgt aatcctctgt aaccattctc 600
ctcaagctct ccacctcac gtccaggctt tggttcctcc agtgggtggc tgtgttggag 660
accattttta caaaattaca tctgaggcac ttcttgttac tcaacagctt gtcaaagtaa 720
ttcgtccttt agatcagcct tctcgtttg atgcaactcc ttatatcaaa gatctattta 780
cctgtaccat taagagatta aaagcagctg acattgatca ggaagtcaag gaaagggcta 840
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atttcctaaa aactttggaa gaccagatt tgaatgtgag aagagtagcc ttggtcacat 2160
ttaattcagc agcacataac aagccatcat taataaggga tctattggat actgttcttc 2220
cacatcttta caatgaaaca aaagttagaa aggagcttat aagagaggta gaaatgggtc 2280
catttaaaaca tacggttgat gatggtctgg atattagaaa ggcagcattt gagtgtatgt 2340
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aagatggttt gaaggaccat tatgatatta agatgctgac atttttaatg ttggtgagac 2460
tgtctaccct ttgtccaagt gcagtactgc agaggttggc ccgacttgtt gagccattac 2520
gtgcaacatg tacaactaag gtaaaggcaa actcagtaaa gcaggagttt gaaaaacaag 2580
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agaagagtcc actgatgagt gaattccagt cacagatcag ttctaaccct gagctggcgg 2700
ctatctttga aagtatccag aaagattcat catctactaa cttggaatca atggacacta 2760

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51/175

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gtagatggt tgttcacat ggggaccatt acatatgacc atacaatgca ctgaattgac 2820
aggtaaatca taagacatgg aaagagaagt gtctaaaagc ttcaaaatgt tccacttttt 2880
tttccttcat ggagactggt tgtttggcgt tcttccattg ttgtttttgt agcatttatt 2940
tcagaaatgt gtatttccat aatccagagg ttgtaaaacc actagtgttt tagtggttac 3000
agcaacattt gaaatggaaa ctagaagtta ggattttatg gagtatggag atagggtcca 3060
gtatctatct accctgtaat gtttaggatt aaaatgttaa aattttgtga c 3111

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<210> 45

<211> 908

<212> PRT

<213> Homo sapiens

<400> 45

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Tyr Ser Asp Asp Asp Asp Met Ser Trp Lys Val Arg Arg Ala Ala Ala
          20          25          30
Lys Cys Leu Asp Ala Val Val Ser Thr Arg His Glu Met Leu Pro Glu
          35          40          45
Phe Tyr Lys Thr Val Ser Pro Ala Leu Ile Ser Arg Phe Lys Glu Arg
          50          55          60
Glu Glu Asn Val Lys Ala Asp Val Phe His Ala Tyr Leu Ser Leu Leu
          65          70          75          80
Lys Gln Thr Arg Pro Val Gln Ser Trp Leu Cys Asp Pro Asp Ala Met
          85          90          95
Glu Gln Gly Glu Thr Pro Leu Thr Met Leu Gln Ser Gln Val Pro Asn
          100          105          110
Ile Val Lys Ala Leu His Lys Gln Met Lys Glu Lys Ser Val Lys Thr
          115          120          125
Arg Gln Cys Cys Phe Asn Ile Leu Thr Glu Leu Val Asn Val Leu Pro
          130          135          140
Gly Ala Leu Thr Gln His Ile Pro Val Leu Val Pro Gly Ile Ile Phe
          145          150          155          160
Ser Leu Asn Asp Lys Ser Ser Ser Ser Asn Leu Lys Ile Asp Ala Leu
          165          170          175
Ser Cys Leu Tyr Val Ile Leu Cys Asn His Ser Pro Gln Val Phe His
          180          185          190
Pro His Val Gln Ala Leu Val Pro Pro Val Val Ala Cys Val Gly Asp
          195          200          205
Pro Phe Tyr Lys Ile Thr Ser Glu Ala Leu Leu Val Thr Gln Gln Leu
          210          215          220
Val Lys Val Ile Arg Pro Leu Asp Gln Pro Ser Ser Phe Asp Ala Thr
          225          230          235          240
Pro Tyr Ile Lys Asp Leu Phe Thr Cys Thr Ile Lys Arg Leu Lys Ala
          245          250          255
Ala Asp Ile Asp Gln Glu Val Lys Glu Arg Ala Ile Ser Cys Met Gly
          260          265          270

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52/175

Gln Ile Ile Cys Asn Leu Gly Asp Asn Leu Gly Ser Asp Leu Pro Asn
 275 280 285
 Thr Leu Gln Ile Phe Leu Glu Arg Leu Lys Asn Glu Ile Thr Arg Leu
 290 295 300
 Thr Thr Val Lys Ala Leu Thr Leu Ile Ala Gly Ser Pro Leu Lys Ile
 305 310 315 320
 Asp Leu Arg Pro Val Leu Gly Glu Gly Val Pro Ile Leu Ala Ser Phe
 325 330 335
 Leu Arg Lys Asn Gln Arg Ala Leu Lys Leu Gly Thr Leu Ser Ala Leu
 340 345 350
 Asp Ile Leu Ile Lys Asn Tyr Ser Asp Ser Leu Thr Ala Ala Met Ile
 355 360 365
 Asp Ala Val Leu Asp Glu Leu Pro Pro Leu Ile Ser Glu Ser Asp Met
 370 375 380
 His Val Ser Gln Met Ala Ile Ser Phe Leu Thr Thr Leu Ala Lys Val
 385 390 395 400
 Tyr Pro Ser Ser Leu Ser Lys Ile Ser Gly Ser Ile Leu Asn Glu Leu
 405 410 415
 Ile Gly Leu Val Arg Ser Pro Leu Leu Gln Gly Gly Ala Leu Ser Ala
 420 425 430
 Met Leu Asp Phe Phe Gln Ala Leu Val Val Thr Gly Thr Asn Asn Leu
 435 440 445
 Gly Tyr Met Asp Leu Leu Arg Met Leu Thr Gly Pro Val Tyr Ser Gln
 450 455 460
 Ser Thr Ala Leu Thr His Lys Gln Ser Tyr Tyr Ser Ile Ala Lys Cys
 465 470 475 480
 Val Ala Ala Leu Thr Arg Ala Cys Pro Lys Glu Gly Pro Ala Val Val
 485 490 495
 Gly Gln Phe Ile Gln Asp Val Lys Asn Ser Arg Ser Thr Asp Ser Ile
 500 505 510
 Arg Leu Leu Ala Leu Leu Ser Leu Gly Glu Val Gly His His Ile Asp
 515 520 525
 Leu Ser Gly Gln Leu Glu Leu Lys Ser Val Ile Leu Glu Ala Phe Ser
 530 535 540
 Ser Pro Ser Glu Glu Val Lys Ser Ala Ala Ser Tyr Ala Leu Gly Ser
 545 550 555 560
 Ile Ser Val Gly Asn Leu Pro Glu Tyr Leu Pro Phe Val Leu Gln Glu
 565 570 575
 Ile Thr Ser Gln Pro Lys Arg Gln Tyr Leu Leu Leu His Ser Leu Lys
 580 585 590
 Glu Ile Ile Ser Ser Ala Ser Val Val Gly Leu Lys Pro Tyr Val Glu
 595 600 605
 Asn Ile Trp Ala Leu Leu Leu Lys His Cys Glu Cys Ala Glu Glu Gly
 610 615 620
 Thr Arg Asn Val Val Ala Glu Cys Leu Gly Lys Leu Thr Leu Ile Asp
 625 630 635 640
 Pro Glu Thr Leu Leu Pro Arg Leu Lys Gly Tyr Leu Ile Ser Gly Ser
 645 650 655



53/175

Ser Tyr Ala Arg Ser Ser Val Val Thr Ala Val Lys Phe Thr Ile Ser
 660 665 670
 Asp His Pro Gln Pro Ile Asp Pro Leu Leu Lys Asn Cys Ile Gly Asp
 675 680 685
 Phe Leu Lys Thr Leu Glu Asp Pro Asp Leu Asn Val Arg Arg Val Ala
 690 695 700
 Leu Val Thr Phe Asn Ser Ala Ala His Asn Lys Pro Ser Leu Ile Arg
 705 710 715 720
 Asp Leu Leu Asp Thr Val Leu Pro His Leu Tyr Asn Glu Thr Lys Val
 725 730 735
 Arg Lys Glu Leu Ile Arg Glu Val Glu Met Gly Pro Phe Lys His Thr
 740 745 750
 Val Asp Asp Gly Leu Asp Ile Arg Lys Ala Ala Phe Glu Cys Met Tyr
 755 760 765
 Thr Leu Leu Asp Ser Cys Leu Asp Arg Leu Asp Ile Phe Glu Phe Leu
 770 775 780
 Asn His Val Glu Asp Gly Leu Lys Asp His Tyr Asp Ile Lys Met Leu
 785 790 795 800
 Thr Phe Leu Met Leu Val Arg Leu Ser Thr Leu Cys Pro Ser Ala Val
 805 810 815
 Leu Gln Arg Leu Asp Arg Leu Val Glu Pro Leu Arg Ala Thr Cys Thr
 820 825 830
 Thr Lys Val Lys Ala Asn Ser Val Lys Gln Glu Phe Glu Lys Gln Asp
 835 840 845
 Glu Leu Lys Arg Ser Ala Thr Arg Ala Val Ala Ala Leu Leu Thr Ile
 850 855 860
 Pro Glu Ala Glu Lys Ser Pro Leu Met Ser Glu Phe Gln Ser Gln Ile
 865 870 875 880
 Ser Ser Asn Pro Glu Leu Ala Ala Ile Phe Glu Ser Ile Gln Lys Asp
 885 890 895
 Ser Ser Ser Thr Asn Leu Glu Ser Met Asp Thr Ser
 900 905

<210> 46

<211> 1599

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (156).. (623)

<400> 46

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 cgccgccgcc cttcgagggc gcccaggcc gcgccatggt gaaggtgacg ttcaactccg 180
 ctctggccca gaaggaggcc aagaaggacg agcccaagag cggcgaggag gcgctcatca 240

54/175

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aaagaagagc ctgggtgttg tgcatgtgct ttggactagc atttatgctt gcaggtgtta 360
ttctaggagg agcatacttg taaaaatatt ttgcacttca accagatgac gtgtactact 420
gtggaataaa gtacatcaaa gatgatgtca tcttaaata gccctctgca gatgcccag 480
ctgctctcta ccagacaatt gaagaaaata ttaaaatctt tgagaagaag aagttgaatt 540
tatcagtgtg cctgtcccag agtttgcaga tagtgatcct gccaacattg ttcatgactt 600
taacaagaaa cttacagcct atttagatct taacctggat aagtgcctat tgatccctct 660
gaacacttcc attgttatgc caccagaaa cctactggag ttacttatta acatcaaggo 720
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tgaaaacatt gatcacctgg gtttctttat ttatcgactg tgtcatgaca aggaaactta 840
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<210> 47

<211> 156

<212> PRT

<213> Homo sapiens

<400> 47

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          20           25           30
Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val Pro Val Gly
          35           40           45
Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala Phe Met
          50           55           60
Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr Phe Ala
          65           70           75           80
Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile Lys Asp
          85           90           95
Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Ala Leu Tyr
          100          105          110
Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Lys Lys Lys Leu Asn
          115          120          125
Leu Ser Val Cys Leu Ser Gln Ser Leu Gln Ile Val Ile Leu Pro Thr

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55/175

130		135		140
Leu Phe Met Thr Leu Thr Arg Asn Leu Gln Pro Ile				
145		150		155

<210> 48
 <211> 3733
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (20).. (1000)

<400> 48

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56/175

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<210> 49

<211> 327

<212> PRT

<213> Homo sapiens

<400> 49

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          20           25           30
Phe Ser Ser Leu Ser Pro Met Ala Arg Lys Ile Met Gln Asp Lys Glu
          35           40           45
Lys Ile Arg Glu Lys Tyr Gly Pro Glu Trp Ala Arg Leu Pro Pro Ala
          50           55           60
Gln Gln Asp Glu Ile Ile Asp Arg Cys Leu Val Gly Pro Arg Ala Pro
          65           70           75           80

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57/175

Ala Pro Arg Asp Pro Gly Asp Ser Glu Glu Leu Thr Arg Ph. Pro Gly
 85 90 95
 Leu Arg Gly Pro Thr Gly Gln Lys Val Val Arg Phe Gly Asp Glu Asp
 100 105 110
 Leu Thr Trp Gln Asp Glu His Ser Ala Pro Phe Ser Trp Glu Thr Lys
 115 120 125
 Ser Gln Met Glu Phe Ser Ile Ser Ala Leu Ser Ile Gln Glu Pro Ser
 130 135 140
 Asn Gly Thr Ala Ala Ser Glu Pro Arg Pro Leu Ser Lys Ala Ser Gln
 145 150 155 160
 Gly Ser Gln Ala Leu Lys Ser Ser Gln Gly Ser Arg Ser Ser Ser Leu
 165 170 175
 Asp Ala Leu Gly Pro Thr Arg Lys Glu Glu Glu Ala Ser Phe Trp Lys
 180 185 190
 Ile Asn Ala Glu Arg Ser Arg Gly Glu Gly Pro Glu Ala Glu Phe Gln
 195 200 205
 Ser Leu Thr Pro Ser Gln Ile Lys Ser Met Glu Lys Gly Glu Lys Val
 210 215 220
 Leu Pro Pro Cys Tyr Arg Gln Glu Pro Ala Pro Lys Asp Arg Glu Ala
 225 230 235 240
 Lys Val Glu Arg Pro Ser Thr Leu Arg Gln Glu Gln Arg Pro Leu Pro
 245 250 255
 Asn Val Ser Thr Glu Arg Glu Arg Pro Gln Pro Val Gln Ala Phe Ser
 260 265 270
 Ser Ala Leu His Glu Ala Ala Pro Ser Gln Leu Glu Gly Lys Leu Pro
 275 280 285
 Ser Pro Asp Val Arg Gln Asp Asp Gly Glu Asp Thr Leu Phe Ser Glu
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 Pro Lys Phe Ala Gln Val Ser Ser Ser Asn Val Val Leu Lys Thr Gly
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 Phe Asp Phe Leu Asp Asn Trp
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<210> 50

<211> 1881

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (141).. (1214)

<400> 50

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58/175

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ctgaatgtgc catttgtctg caaacatgtg ttcattccagt cagtctgccc tgtaagcacg 300
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cttatgtttc agaattgttg taacacactt catggtgttc ccataggctt tgcgtcttag 1800
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<210> 51

<211> 358

<212> PRT

<213> Homo sapiens

<400> 51

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          20          25          30
Val Pro Glu Cys Ala Ile Cys Leu Gln Thr Cys Val His Pro Val Ser
          35          40          45
Leu Pro Cys Lys His Val Phe Cys Tyr Leu Cys Val Lys Gly Ala Ser
          50          55          60
Trp Leu Gly Lys Arg Cys Ala Leu Arg Arg Gln Glu Ile Pro Glu Asp
          65          70          75          80
Phe Leu Asp Lys Pro Thr Leu Leu Ser Pro Glu Glu Leu Lys Ala Ala
          85          90          95

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59/175

Ser Arg Gly Asn Gly Glu Tyr Ala Trp Tyr Tyr Glu Gly Arg Asn Gly
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 Trp Trp Gln Tyr Asp Glu Arg Thr Ser Arg Glu Leu Glu Asp Ala Phe
 115 120 125
 Ser Lys Gly Lys Lys Asn Thr Glu Met Leu Ile Ala Gly Phe Leu Tyr
 130 135 140
 Val Ala Asp Leu Glu Asn Met Val Gln Tyr Arg Arg Asn Glu His Gly
 145 150 155 160
 Arg Arg Arg Lys Ile Lys Arg Asp Ile Ile Asp Ile Pro Lys Lys Gly
 165 170 175
 Val Ala Gly Leu Arg Leu Asp Cys Asp Ala Asn Thr Val Asn Leu Ala
 180 185 190
 Arg Glu Ser Ser Ala Asp Gly Ala Asp Ser Val Ser Ala Gln Ser Gly
 195 200 205
 Ala Ser Val Gln Pro Leu Val Ser Ser Val Arg Pro Leu Thr Ser Val
 210 215 220
 Asp Gly Gln Ser Thr Ser Pro Ala Thr Pro Ser Pro Asp Ala Ser Thr
 225 230 235 240
 Ser Leu Glu Asp Ser Phe Ala His Leu Gln Leu Ser Gly Asp Asn Thr
 245 250 255
 Ala Glu Arg Ser His Arg Gly Glu Gly Glu Glu Asp His Glu Ser Pro
 260 265 270
 Ser Ser Gly Arg Val Pro Ala Pro Asp Thr Ser Ile Glu Glu Thr Glu
 275 280 285
 Ser Asp Ala Ser Ser Asp Ser Glu Asp Val Ser Ala Val Val Ala Gln
 290 295 300
 His Ser Leu Thr Gln Gln Arg Leu Leu Val Ser Asn Ala Asn Gln Thr
 305 310 315 320
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<210> 52

<211> 1824

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (208).. (1824)

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60/175

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ggcaaaaccc cctctaagga gaag 1824

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<210> 53

<211> 539

<212> PRT

<213> Homo sapiens

<400> 53

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          20           25           30
Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg Glu Leu Pro
        35           40           45
Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn Tyr Arg Asp
        50           55           60
Met Gly Glu His Arg Val Ile Leu Pro Asp Asp Val Arg Asp Phe Ile
        65           70           75           80
Asp Asn Leu Asp Arg Pr Pro Gly Ser Ser Tyr Phe Arg Tyr Ala Glu

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61/175

85												90			95		
Ser	Ser	Met	Lys	Asn	Ser	Phe	Gly	Leu	Lys	Tyr	Leu	His	Lys	Phe	Phe		
			100				105						110				
Asn	Ile	Pro	Ser	Leu	Gln	Leu	Gln	Arg	Glu	Thr	Leu	Leu	Arg	Gln	Leu		
		115				120						125					
Glu	Thr	Asn	Gln	Leu	Asp	Met	Asp	Ala	Thr	Leu	Glu	Glu	Leu	Ser	Val		
		130				135						140					
Gln	Gln	Glu	Thr	Glu	Asp	Gln	Asn	Tyr	Gly	Ile	Phe	Leu	Glu	Met	Met		
145				150			155						160				
Glu	Ala	Arg	Ser	Arg	Gly	His	Ala	Ser	Pro	Leu	Ala	Ala	Asn	Gly	Gln		
			165			170						175					
Ser	Pro	Ser	Pro	Gly	Ser	Gln	Ser	Pro	Val	Val	Pro	Ala	Gly	Ala	Val		
			180			185						190					
Ser	Thr	Gly	Ser	Ser	Ser	Pro	Gly	Thr	Pro	Gln	Pro	Ala	Pro	Gln	Leu		
		195				200						205					
Pro	Leu	Asn	Ala	Ala	Pro	Pro	Ser	Ser	Val	Pro	Pro	Val	Pro	Pro	Ser		
		210				215						220					
Glu	Ala	Leu	Pro	Pro	Pro	Ala	Cys	Pro	Ser	Ala	Pro	Ala	Pro	Arg	Arg		
225				230			235						240				
Ser	Ile	Ile	Ser	Arg	Leu	Phe	Gly	Thr	Ser	Pro	Ala	Thr	Glu	Ala	Ala		
			245			250						255					
Pro	Pro	Pro	Pro	Glu	Pro	Val	Pro	Ala	Ala	Gln	Gly	Pro	Ala	Thr	Val		
			260			265						270					
Gln	Ser	Val	Glu	Asp	Phe	Val	Pro	Asp	Asp	Arg	Leu	Asp	Arg	Ser	Phe		
		275				280						285					
Leu	Glu	Asp	Thr	Thr	Pro	Ala	Arg	Asp	Glu	Lys	Lys	Val	Gly	Ala	Lys		
		290				295						300					
Ala	Ala	Gln	Gln	Asp	Ser	Asp	Ser	Asp	Gly	Glu	Ala	Leu	Gly	Gly	Asn		
305				310			315						320				
Pro	Met	Val	Ala	Gly	Phe	Gln	Asp	Asp	Val	Asp	Leu	Glu	Asp	Gln	Pro		
			325			330						335					
Arg	Gly	Ser	Pro	Pro	Leu	Pro	Ala	Gly	Pro	Val	Pro	Ser	Gln	Asp	Ile		
			340			345						350					
Thr	Leu	Ser	Ser	Glu	Glu	Glu	Ala	Glu	Val	Ala	Ala	Pro	Thr	Lys	Gly		
		355				360						365					
Pro	Ala	Pro	Ala	Pro	Gln	Gln	Cys	Ser	Glu	Pro	Glu	Thr	Lys	Trp	Ser		
		370				375						380					
Ser	Ile	Pro	Ala	Ser	Lys	Pro	Arg	Arg	Gly	Thr	Ala	Pro	Thr	Arg	Thr		
385				390			395						400				
Ala	Ala	Pro	Pro	Trp	Pro	Gly	Gly	Val	Ser	Val	Arg	Thr	Gly	Pro	Glu		
			405			410						415					
Lys	Arg	Ser	Ser	Thr	Arg	Pro	Pro	Ala	Glu	Met	Glu	Pro	Gly	Lys	Gly		
			420			425						430					
Glu	Gln	Ala	Ser	Ser	Ser	Glu	Ser	Asp	Pro	Glu	Gly	Pro	Ile	Ala	Ala		
		435				440						445					
Gln	Met	Leu	Ser	Phe	Val	Met	Asp	Asp	Pro	Asp	Phe	Glu	Ser	Glu	Gly		
		450				455						460					
Ser	Asp	Thr	Gln	Arg	Arg	Ala	Asp	Asp	Phe	Pro	Val	Arg	Asp	Asp	Pro		

62/175

465				470					475				480
Ser	Asp	Val	Thr	Asp	Glu	Asp	Glu	Gly	Pro	Ala	Glu	Pro	Pro
				485					490				495
Pro	Lys	Leu	Pro	Leu	Pro	Ala	Phe	Arg	Leu	Lys	Asn	Asp	Ser
			500					505				510	Asp
Phe	Gly	Leu	Gly	Leu	Glu	Glu	Ala	Gly	Pro	Lys	Glu	Ser	Glu
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	530					535							

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 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> (8).. (1432)

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63/175

<210> 55
 <211> 475
 <212> PRT
 <213> Homo sapiens

<400> 55

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		20					25					30			
Gln	Ile	Thr	Pro	Asp	Lys	Ile	Gln	Phe	Glu	Arg	Asn	Phe	Asp	Arg	Gln
	35					40					45				
Lys	Ser	Arg	Ile	Leu	Ser	Leu	Ser	Trp	His	Pro	Ser	Gly	Thr	His	Ile
	50					55					60				
Ala	Ala	Gly	Ser	Ile	Asp	Tyr	Ile	Ser	Val	Phe	Asp	Val	Lys	Ser	Gly
65					70					75					80
Ser	Ala	Val	His	Lys	Met	Ile	Val	Asp	Arg	Gln	Tyr	Met	Gly	Val	Ser
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Lys	Arg	Lys	Cys	Ile	Val	Trp	Gly	Val	Ala	Phe	Leu	Ser	Asp	Gly	Thr
			100					105					110		
Ile	Ile	Ser	Val	Asp	Ser	Ala	Gly	Lys	Val	Gln	Phe	Trp	Asp	Ser	Ala
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Thr	Gly	Thr	Leu	Val	Lys	Ser	His	Leu	Ile	Ala	Asn	Ala	Asp	Val	Gln
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Glu	Gly	Thr	Val	Phe	His	Phe	Gln	Leu	Val	Pro	Val	Thr	Ser	Asn	Ser
				165					170					175	
Ser	Glu	Lys	Gln	Trp	Val	Arg	Thr	Lys	Pro	Phe	Gln	His	His	Thr	His
			180					185					190		
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Thr	Asp	Thr	His	Leu	Val	Phe	Arg	Pro	Leu	Met	Glu	Lys	Val	Glu	Val
	210					215					220				
Lys	Asn	Tyr	Asp	Ala	Ala	Leu	Arg	Lys	Ile	Thr	Phe	Pro	His	Arg	Cys
225				230						235					240
Leu	Ile	Ser	Cys	Ser	Lys	Lys	Arg	Gln	Leu	Leu	Leu	Phe	Gln	Phe	Ala
				245					250					255	
His	His	Leu	Glu	Leu	Trp	Arg	Leu	Gly	Ser	Thr	Val	Ala	Thr	Gly	Thr
			260					265					270		
Val	Glu	Ala	Met	Cys	Leu	Leu	Ala	Val	Ser	Pro	Asp	Gly	Asn	Trp	Leu
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Ala	Ala	Ser	Gly	Thr	Ser	Ala	Gly	Val	His	Val	Tyr	Asn	Val	Lys	Gln
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Leu	Lys	Leu	His	Cys	Thr	Val	Pro	Ala	Tyr	Asn	Phe	Pro	Val	Thr	Ala
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Met	Ala	Ile	Ala	Pro	Asn	Thr	Asn	Asn	Leu	Val	Ile	Ala	His	Ser	Asp

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<div> <div>340</div> <div>345</div> <div>350</div> </div>															
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Ile	Leu	Leu	His	Asp	Ala	Tyr	Met	Phe	Cys	Ile	Ile	Asp	Lys	Ser	Leu
<div> <div>385</div> <div>390</div> <div>395</div> </div>															
Pro	Leu	Pro	Asn	Asp	Lys	Thr	Leu	Leu	Tyr	Asn	Pro	Phe	Pro	Pro	Thr
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Asn	Glu	Ser	Asp	Val	Ile	Arg	Arg	Arg	Thr	Ala	His	Ala	Phe	Lys	Ile
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<210> 56
 <211> 2176
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (26).. (709)

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ccggggcatg	cacggcatgc	tcaaggtgct	gtacggcacc	gtgcgcatca	gctgcatgga	300
caagctagac	gcggggcgcg	ggcaacggcc	gocggccttg	ccgcccagac	agcagttcga	360
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cgagtacacc	gaggccagcg	gccctgcat	cctcacaccg	caccggggaca	acctgcacca	480
gatcgacgcc	gtggaagggc	ctgccgcctt	cctggacatc	ctggccccgc	cctacgacct	540
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65/175

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gtttaaggag atgagctact gtttaaagtg agctggcctg cctaattaat tccttgtgaa 1260
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2176

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<210> 57

<211> 228

<212> PRT

<213> Homo sapiens

<400> 57

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          20          25          30
Leu Gln Pro Leu Pro Pro Asn Leu Pro Pro Val Thr Tyr Met His Ile
          35          40          45
Tyr Glu Thr Asp Gly Phe Ser Leu Gly Val Phe Leu Leu Lys Ser Gly
          50          55          60
Thr Ser Ile Pro Leu His Asp His Pro Gly Met His Gly Met Leu Lys
          65          70          75          80
Val Leu Tyr Gly Thr Val Arg Ile Ser Cys Met Asp Lys Leu Asp Ala
          85          90          95
Gly Gly Gly Gln Arg Pro Arg Ala Leu Pro Pro Glu Gln Gln Phe Glu
          100         105         110
Pro Pro Leu Gln Pro Arg Glu Arg Glu Ala Val Arg Pro Gly Val Leu
          115         120         125
Arg Ser Arg Ala Glu Tyr Thr Glu Ala Ser Gly Pro Cys Ile Leu Thr
          130         135         140
Pro His Arg Asp Asn Leu His Gln Ile Asp Ala Val Glu Gly Pro Ala
          145         150         155         160

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66/175

Ala	Phe	Leu	Asp	Ile	Leu	Ala	Pro	Pro	Tyr	Asp	Pro	Asp	Asp	Gly	Arg	
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Asp	Cys	His	Tyr	Tyr	Arg	Val	Leu	Glu	Pro	Val	Arg	Pro	Lys	Glu	Ala	
				180					185					190		
Ser	Ser	Ser	Ala	Cys	Asp	Leu	Pro	Arg	Glu	Val	Trp	Leu	Leu	Glu	Thr	
				195					200					205		
Pro	Gln	Ala	Asp	Asp	Phe	Trp	Cys	Glu	Gly	Glu	Pro	Tyr	Pro	Gly	Pro	
				210					215					220		
Lys	Val	Phe	Pro													
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<210> 58
 <211> 2661
 <212> DNA
 <213> Homo sapiens

<220>
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67/175

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<210> 59

<211> 680

<212> PRT

<213> Homo sapiens

<400> 59

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Pro Val Val Glu Gly Pro Pro Pro Gly Leu Pro Pro Pro Pro Pro
      35             40             45
Ile Leu Thr Pro Pro Pro Val Asn Leu Arg Pro Pro Val Pro Pro Pro
      50             55             60
Gly Pro Leu Pro Pro Ser Leu Pro Pro Val Thr Gly Pro Pro Pro Pro
      65             70             75             80
Leu Pro Pro Leu Gln Pro Ser Gly Met Asp Ala Pro Pro Asn Ser Ala
      85             90             95
Thr Ser Ser Val Pro Thr Val Val Thr Thr Gly Ile His His Gln Pro
      100             105             110
Pro Pro Ala Pro Pro Ser Leu Phe Thr Ala Asp Thr Tyr Asp Thr Asp
      115             120             125
Gly Tyr Asn Pro Glu Ala Pro Ser Ile Thr Asn Thr Ser Arg Pro Met
      130             135             140
Tyr Arg His Arg Val His Ala Gln Arg Pro Asn Leu Ile Gly Leu Thr
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Ser Gly Asp Met Asp Leu Pro Pro Arg Glu Lys Pro Pro Asn Lys Ser

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68/175

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Ser	Met	Arg	Ile	Val	Val	Asp	Ser	Glu	Ser	Arg	Lys	Arg	Thr	Ile	Gly		
			180					185					190				
Ser	Gly	Glu	Pro	Gly	Val	Pro	Thr	Lys	Lys	Thr	Trp	Phe	Asp	Lys	Pro		
		195					200					205					
Asn	Phe	Asn	Arg	Thr	Asn	Ser	Pro	Gly	Phe	Gln	Lys	Lys	Val	Gln	Phe		
	210					215					220						
Gly	Asn	Glu	Asn	Thr	Lys	Leu	Glu	Leu	Arg	Lys	Val	Pro	Pro	Glu	Leu		
225					230					235					240		
Asn	Asn	Ile	Ser	Lys	Leu	Asn	Glu	His	Phe	Ser	Arg	Phe	Gly	Thr	Leu		
				245					250					255			
Val	Asn	Leu	Gln	Val	Ala	Tyr	Asn	Gly	Asp	Pro	Glu	Gly	Ala	Leu	Ile		
			260					265					270				
Gln	Phe	Ala	Thr	Tyr	Glu	Glu	Ala	Lys	Lys	Ala	Ile	Ser	Ser	Thr	Glu		
		275					280					285					
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	290					295					300						
Ser	Thr	Gln	Gln	Leu	Gln	Thr	Thr	Ser	Pro	Lys	Val	Met	Gln	Pro	Leu		
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Val	Gln	Gln	Pro	Ile	Leu	Pro	Val	Val	Lys	Gln	Ser	Val	Lys	Glu	Arg		
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Leu	Gly	Pro	Val	Pro	Ser	Ser	Thr	Ile	Glu	Pro	Ala	Glu	Ala	Gln	Ser		
			340					345					350				
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		355					360					365					
Lys	Thr	Val	Tyr	Asn	Pro	Ala	Ala	Leu	Lys	Ala	Ala	Gln	Lys	Thr	Leu		
	370					375					380						
Leu	Val	Ser	Thr	Ser	Ala	Val	Asp	Asn	Asn	Glu	Ala	Gln	Lys	Lys	Lys		
385					390					395					400		
Gln	Glu	Ala	Leu	Lys	Leu	Gln	Gln	Asp	Val	Arg	Lys	Arg	Lys	Gln	Glu		
				405					410					415			
Ile	Leu	Glu	Lys	His	Ile	Glu	Thr	Gln	Lys	Met	Leu	Ile	Ser	Lys	Leu		
			420					425				430					
Glu	Lys	Asn	Lys	Thr	Met	Lys	Ser	Glu	Asp	Lys	Ala	Glu	Ile	Met	Lys		
		435					440					445					
Thr	Leu	Glu	Val	Leu	Thr	Lys	Asn	Ile	Thr	Lys	Leu	Lys	Asp	Glu	Val		
	450					455						460					
Lys	Ala	Ala	Ser	Pro	Gly	Arg	Cys	Leu	Pro	Lys	Ser	Ile	Lys	Thr	Lys		
465					470					475					480		
Thr	Gln	Met	Gln	Lys													

69/175

545		550		555		560
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	580	585	590			
Gln Ile Asp Asp	Ser Ser Leu His Ala Val Ile Thr Phe Lys Thr	Arg				
	595	600	605			
Ala Glu Ala Glu	Ala Ala Ala Val His Gly Ala Arg Phe Lys Gly Gln					
	610	615	620			
Asp Leu Lys Leu	Ala Trp Asn Lys Pro Val Thr Asn Ile Ser	Ala Val				
625	630	635	640			
Glu Thr Glu Glu	Val Gly Pro Asp Glu Glu Glu Phe Gln Glu Glu	Ser				
	645	650	655			
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<210> 60

<211> 2005

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (137).. (844)

<400> 60

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gcctcctcag gaggagcatt agtagaacag cagtgtatgag gacacagagg gagcagacag 1080
tggttaccac gatctccgta accatttgca tgtgacttag caagggctct gaaatgacaa 1140

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70/175

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agctttaact gtattgggaa aacttaaaaa atagcatcct caaatTTTct gattcTTatt 1260
tgccatgaaa tagaacttag taaattaaat gttatttgaa aatgttataa gagctttgta 1320
aatatttcag aaaatatggg ataaatgcct gaatttgggt cttctacagg tgctataata 1380
aagtccatct ctcaatactt atactttcta aattcatctc agaataattag cagccatatt 1440
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ttccaatcct tcaaaatatt attgtgtatc ttaagaagta taggaacttg tatgttgaaa 1560
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<210> 61

<211> 236

<212> PRT

<213> Homo sapiens

<400> 61

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Leu Ile Ile Gln Ser Leu Gln Arg Gly Asp Ile Gln Pro Trp Leu His
      20             25             30
Ser Gly Ser Asn Ser Leu Leu Ser Lys Leu Ile His Gln Ser Tyr His
      35             40             45
Gly Thr Met Asp Thr Val Ser Leu Ser Gly Thr Ile Pro Val Gln Met
      50             55             60
Leu Leu Glu Ile Gly Leu Asp Lys Leu Lys Lys Asp Tyr Ile Ser Phe
      65             70             75             80
Phe Ile Gly Gln Glu Leu Ala Ser Leu Asn His Leu Glu Tyr Phe Ile
      85             90             95
Ala Pro Ser Val Asp Ile Gln Glu Gln Val Tyr Arg Val Gln Lys Leu
      100            105            110
His His Ile Leu Glu Ile Leu Val Ser Cys Met Pro Phe Ile Lys Ser
      115            120            125
Gln His Glu Leu Leu Phe Ser Leu Thr Gln Ile Cys Ile Lys Tyr Tyr
      130            135            140
Lys Gln Asn Pro Leu Asp Glu Gln His Ile Phe Gln Leu Pro Val Arg
      145            150            155            160
Pro Thr Ala Val Lys Asn Leu Tyr Gln Ser Glu Lys Pro Gln Lys Trp
      165            170            175
Arg Val Glu Ile Tyr Ser Gly Gln Lys Lys Ile Lys Thr Val Trp Gln
      180            185            190
Leu Ser Asp Ser Ser Pro Ile Asp His Leu Asn Phe His Lys Pro Asp

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71/175

	195		200		205										
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Thr	Asn	Met	Val	Thr	Cys	Ser	Gln	Val	His	Phe	Lys				
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<210> 62
 <211> 2279
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (97).. (1650)

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 gtatcccttt ccatgaccog acctgtgtct attgaggggt ccgaggaata ccagcgttaag 180
 cacctagcag cccatgggtt aacgatgctg tttagcaca tggccacaaa ttacaagctt 240
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 gattataata ccctacagga agcactaagt aatatggatg attatgacaa aacctgcttg 360
 gagtctgcat tagtttgtgt ttgcaatata gttcagcaag aatgggggtg tgcaattcct 420
 tgccagggtg tcctgggtgac agacggctgt cttggcattg gtagagggtc actgcgacat 480
 tccctagcca ctcaaaatca acgaagttag agcaacaggt ttccactacc ttttccttc 540
 ccatctaagt tatatatcat gtgcatggcg aatttggagg agctccagag caccgattcc 600
 ttggaatgcc ttgaacgtct catatattta aacaatgggt aagggcagat ttttactatt 660
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 cccaggccag aaccttttgt tgtagatgaa gaaattgatc ctatccctaa agtcattaac 840
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 tccagacatc tggctttacc tatagcactt aacaaagaag gtgatgaggt gggactggc 960
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 ctactagtat gagaaggatg tgaaggtggg tggctggttg ggctttaact tcctgggatt 1860

72/175

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 ctttaagtgt tttggtatct cttgagattc taacttttaa agagcaacca ttaatgtgta 2220
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<210> 63

<211> 518

<212> PRT

<213> Homo sapiens

<400> 63

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			20					25					30		
His	Gly	Leu	Thr	Met	Leu	Phe	Glu	His	Met	Ala	Thr	Asn	Tyr	Lys	Leu
		35					40					45			
Glu	Phe	Thr	Ala	Leu	Val	Val	Phe	Ser	Ser	Leu	Trp	Glu	Leu	Met	Val
	50					55				60					
Pro	Phe	Thr	Arg	Asp	Tyr	Asn	Thr	Leu	Gln	Glu	Ala	Leu	Ser	Asn	Met
	65				70					75				80	
Asp	Asp	Tyr	Asp	Lys	Thr	Cys	Leu	Glu	Ser	Ala	Leu	Val	Gly	Val	Cys
				85					90					95	
Asn	Ile	Val	Gln	Gln	Glu	Trp	Gly	Gly	Ala	Ile	Pro	Cys	Gln	Val	Val
		100					105						110		
Leu	Val	Thr	Asp	Gly	Cys	Leu	Gly	Ile	Gly	Arg	Gly	Ser	Leu	Arg	His
	115					120						125			
Ser	Leu	Ala	Thr	Gln	Asn	Gln	Arg	Ser	Glu	Ser	Asn	Arg	Phe	Pro	Leu
	130					135					140				
Pro	Phe	Pro	Phe	Pro	Ser	Lys	Leu	Tyr	Ile	Met	Cys	Met	Ala	Asn	Leu
	145				150					155				160	
Glu	Glu	Leu	Gln	Ser	Thr	Asp	Ser	Leu	Glu	Cys	Leu	Glu	Arg	Leu	Ile
			165					170						175	
Tyr	Leu	Asn	Asn	Gly	Glu	Gly	Gln	Ile	Phe	Thr	Ile	Asp	Gly	Pro	Leu
		180					185						190		
Cys	Leu	Lys	Asn	Val	Gln	Ser	Met	Phe	Gly	Lys	Leu	Ile	Asp	Leu	Ala
	195						200					205			
Tyr	Thr	Pro	Phe	His	Ala	Val	Leu	Lys	Cys	Gly	His	Leu	Thr	Ala	Asp
	210					215					220				
Val	Gln	Val	Phe	Pro	Arg	Pro	Glu	Pro	Phe	Val	Val	Asp	Glu	Glu	Ile
	225				230					235				240	
Asp	Pro	Ile	Pro	Lys	Val	Ile	Asn	Thr	Asp	Leu	Glu	Ile	Val	Gly	Phe
			245					250					255		
Ile	Asp	Ile	Ala	Asp	Ile	Ser	Ser	Pro	Pro	Val	Leu	Ser	Arg	His	Leu

73/175

260										265				270			
Val	Leu	Pro	Ile	Ala	Leu	Asn	Lys	Glu	Gly	Asp	Glu	Val	Gly	Thr	Gly		
		275					280					285					
Ile	Thr	Asp	Asp	Asn	Glu	Asp	Glu	Asn	Ser	Ala	Asn	Gln	Ile	Ala	Gly		
290						295					300						
Lys	Ile	Pro	Asn	Phe	Cys	Val	Leu	Leu	His	Gly	Ser	Leu	Lys	Val	Glu		
305					310					315			320				
Gly	Met	Val	Ala	Ile	Val	Gln	Leu	Gly	Pro	Glu	Trp	His	Gly	Met	Leu		
				325					330					335			
Tyr	Ser	Gln	Ala	Asp	Ser	Lys	Lys	Lys	Ser	Asn	Leu	Met	Met	Ser	Leu		
		340						345					350				
Phe	Glu	Pro	Gly	Pro	Glu	Pro	Leu	Pro	Trp	Leu	Gly	Lys	Met	Ala	Gln		
355						360						365					
Leu	Gly	Pro	Ile	Ser	Asp	Ala	Lys	Glu	Asn	Pro	Tyr	Gly	Glu	Asp	Asp		
370						375					380						
Asn	Lys	Ser	Pro	Phe	Pro	Leu	Gln	Pro	Lys	Asn	Lys	Arg	Ser	Tyr	Ala		
385					390					395			400				
Gln	Asn	Val	Thr	Val	Trp	Ile	Lys	Pro	Ser	Gly	Leu	Gln	Thr	Asp	Val		
				405					410					415			
Gln	Lys	Ile	Leu	Arg	Asn	Ala	Arg	Lys	Leu	Pro	Glu	Lys	Thr	Gln	Thr		
		420						425					430				
Phe	Tyr	Lys	Glu	Leu	Asn	Arg	Leu	Arg	Lys	Ala	Ala	Leu	Ala	Phe	Gly		
435						440						445					
Phe	Leu	Asp	Leu	Leu	Lys	Gly	Val	Ala	Asp	Met	Leu	Glu	Arg	Glu	Cys		
450						455					460						
Thr	Leu	Leu	Pro	Glu	Thr	Ala	His	Pro	Asp	Ala	Ala	Phe	Gln	Leu	Thr		
465					470					475			480				
His	Ala	Ala	Gln	Gln	Leu	Lys	Leu	Ala	Ser	Thr	Gly	Thr	Ser	Glu	Tyr		
				485					490					495			
Ala	Ala	Tyr	Asp	Gln	Asn	Ile	Thr	Pro	Leu	His	Thr	Asp	Phe	Ser	Gly		
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Ser	Ser	Thr	Glu	Arg	Ile												
515																	

<210> 64
 <211> 2155
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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cccgcacgca atctgcctcg gagacgttga taacgatacg ttaaataaac tgggtggtggg 180

74/175

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cctgtttggtg gcagtgagtg ctgaaggctg gtttcatttg tttagacctga cacctgccaa 360
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ccttctcagc ttgccgtatt cttcaggtat tagtcagctt cagaagccct gctcccattt 2040
ttccaccac ccattcccc ataaaacagc ttattgtctc caagacaata gacatttaaa 2100
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<210> 65

<211> 447

<212> PRT

<213> Homo sapiens

<400> 65

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Ser Leu Phe Pro His Ala Ile Cys Leu Gly Asp Val Asp Asn Asp Thr
          20           25           30
Leu Asn Glu Leu Val Val Gly Asp Thr Ser Gly Lys Val Ser Val Tyr
          35           40           45
Lys Asn Asp Asp Ser Arg Pro Trp Leu Thr Cys Ser Cys Gln Gly Met

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75/175

50	55	60
Leu Thr Cys Ala Gly Val Gly Asp Val Cys Asn Lys Gly Lys Asn Leu		
65	70	75
Leu Val Ala Val Ser Ala Glu Gly Trp Phe His Leu Phe Asp Leu Thr		80
	85	90
Pro Ala Lys Val Leu Asp Ala Ser Gly His His Glu Thr Leu Ile Gly		95
	100	105
Glu Glu Gln Arg Pro Val Phe Lys Gln His Ile Pro Ala Asn Thr Lys		110
	115	120
Val Met Leu Ile Ser Asp Ile Asp Gly Asp Gly Cys Arg Glu Leu Val		125
	130	135
Val Gly Tyr Thr Asp Arg Val Val Arg Ala Phe Arg Trp Glu Glu Leu		140
145	150	155
Gly Glu Gly Pro Glu His Leu Thr Gly Gln Leu Val Ser Leu Lys Lys		160
	165	170
Trp Met Leu Glu Gly Gln Val Asp Ser Leu Ser Val Thr Leu Gly Pro		175
	180	185
Leu Gly Leu Pro Glu Leu Met Val Ser Gln Pro Gly Cys Ala Tyr Ala		190
	195	200
Ile Leu Leu Cys Thr Trp Lys Lys Asp Thr Gly Ser Pro Pro Ala Ser		205
	210	215
Glu Gly Pro Thr Asp Gly Ser Arg Glu Thr Pro Ala Ala Arg Asp Val		220
225	230	235
Val Leu His Gln Thr Ser Gly Arg Ile His Asn Lys Asn Val Ser Thr		240
	245	250
His Leu Ile Gly Asn Ile Lys Gln Gly His Gly Thr Glu Ser Ser Gly		255
	260	265
Ser Gly Leu Phe Ala Leu Cys Thr Leu Asp Gly Thr Leu Lys Leu Met		270
	275	280
Glu Glu Met Glu Glu Ala Asp Lys Leu Leu Trp Ser Val Gln Val Asp		285
	290	295
His Gln Leu Phe Ala Leu Glu Lys Leu Asp Val Thr Gly Asn Gly His		300
305	310	315
Glu Glu Val Val Ala Cys Ala Trp Asp Gly Gln Thr Tyr Ile Ile Asp		320
	325	330
His Asn Arg Thr Val Val Arg Phe Gln Val Asp Glu Asn Ile Arg Ala		335
	340	345
Phe Cys Ala Gly Leu Tyr Ala Cys Lys Glu Gly Arg Asn Ser Pro Cys		350
	355	360
Leu Val Tyr Val Thr Phe Asn Gln Lys Ile Tyr Val Tyr Trp Glu Val		365
	370	375
Gln Leu Glu Arg Met Glu Ser Thr Asn Leu Val Lys Leu Leu Glu Thr		380
385	390	395
Lys Pro Glu Tyr His Ser Leu Leu Gln Glu Leu Gly Val Asp Pro Asp		400
	405	410
Asp Leu Pr Val Thr Arg Ala Leu Leu His Gln Thr Leu Tyr His Pro		415
	420	425
Asp Gln Pro Pro Gln Cys Ala Pro Ser Ser Leu Gln Asp Pro Thr		430

76/175

435

440

445

<210> 66
 <211> 1793
 <212> DNA
 <213> Homo sapiens

<220>
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 tgactgtttc ttggggcttc atgacagaaa gatgtgtgtt ctoggactct gtgctcttat 180
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 agatggagat gatgaagatt gggaagaaga tgatgctgaa gagactgctc tggaaggcta 480
 ttccacaatc attgatgatg aagataaccc tgttgatgag tatcagatat ttaaagctat 540
 ctttcaaact attcaaaaac gtaatcctgt gtggtatcag gcactgactc acggtcttaa 600
 tgaagaacaa agaaaacagt tacaggacat agcaactctg gctgatcaaa gaagagcagc 660
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 gcttttcttt ttctgaggaa aaaataggca tgggctacag gactatttaa aatgtctcat 1140
 ttacagtata aaactcaaag gtagatgtaa tttttacacc tatgagtatt tgtccaattt 1200
 ctgtctcttc ctaccattg ggtatctatt ctttatatgt aaataagata aggtcatctg 1260
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<210> 67
 <211> 203
 <212> PRT

77/175

<213> Homo sapiens

<400> 67

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 20          25          30
Leu Phe Asn Gly Leu Lys Arg Ala Tyr Ala Cys His Ala Glu His Glu
 35          40          45
Asn Asp Ser Asp Asp Asp Asp Glu Ala Glu Asp Asp Asp Glu Thr Glu
 50          55          60
Glu Leu Gly Ser Asp Glu Asp Asp Ile Asp Glu Asp Gly Gln Glu Tyr
 65          70          75          80
Leu Glu Ile Leu Ala Lys Gln Ala Gly Glu Asp Gly Asp Asp Glu Asp
 85          90          95
Trp Glu Glu Asp Asp Ala Glu Glu Thr Ala Leu Glu Gly Tyr Ser Thr
100          105          110
Ile Ile Asp Asp Glu Asp Asn Pro Val Asp Glu Tyr Gln Ile Phe Lys
115          120          125
Ala Ile Phe Gln Thr Ile Gln Asn Arg Asn Pro Val Trp Tyr Gln Ala
130          135          140
Leu Thr His Gly Leu Asn Glu Glu Gln Arg Lys Gln Leu Gln Asp Ile
145          150          155          160
Ala Thr Leu Ala Asp Gln Arg Arg Ala Ala His Glu Ser Lys Met Ile
165          170          175
Glu Lys His Gly Gly Tyr Lys Phe Ser Ala Pro Val Val Pro Ser Ser
180          185          190
Phe Asn Phe Gly Gly Pro Ala Pro Gly Met Asn
195          200

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<210> 68

<211> 2160

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (115).. (1146)

<400> 68

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agaggcgctg ccagacccc gggatcgggtg gaggaagatg ctttgctctg tggacccgtg 360
agcaagcata agctgccaac ccaagggtgag gacagacgag tgccacaaaa ctggtttcct 420

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78/175

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aaacaacagg ttttcttggt ggagagggtg aaacagcgga tgattctgga actgggagaa 600
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<210> 69

<211> 344

<212> PRT

<213> Homo sapiens

<400> 69

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          20           25           30
Tyr Ser Cys Gly Arg Lys Lys Lys Val Asn Pro Tyr Glu Glu Val Asp
          35           40           45
Gln Glu Lys Tyr Ser Asn Leu Val Gln Ser Val Leu Ser Ser Arg Gly
          50           55           60
Val Ala Gln Thr Pro Gly Ser Val Glu Glu Asp Ala Leu Leu Cys Gly
          65           70           75           80
Pro Val Ser Lys His Lys Leu Pro Asn Gln Gly Glu Asp Arg Arg Val

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				85					90					95	
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Asn	Ala	Ser	Asp	Pro	Ser	Val	Pro	Leu	Lys	Ile	Pro	Leu	Gln	Arg	Asn
115				120				125							
Val	Ile	Pro	Ser	Val	Thr	Arg	Val	Leu	Gln	Gln	Thr	Met	Thr	Lys	Gln
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Gln	Val	Phe	Leu	Leu	Glu	Arg	Trp	Lys	Gln	Arg	Met	Ile	Leu	Glu	Leu
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Gly	Glu	Asp	Gly	Phe	Lys	Glu	Tyr	Thr	Ser	Asn	Val	Phe	Leu	Gln	Gly
165				170				175							
Lys	Arg	Phe	His	Glu	Ala	Leu	Glu	Ser	Ile	Leu	Ser	Pro	Gln	Glu	Thr
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Leu	Lys	Glu	Arg	Asp	Glu	Asn	Leu	Leu	Lys	Ser	Gly	Tyr	Ile	Glu	Ser
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Val	Gln	His	Ile	Leu	Lys	Asp	Val	Ser	Gly	Val	Arg	Ala	Leu	Glu	Ser
210				215				220							
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245				250				255							
Lys	Pro	Lys	Pro	Phe	Ile	Gln	Ser	Thr	Phe	Asp	Asn	Pro	Leu	Gln	Val
260				265				270							
Val	Ala	Tyr	Met	Gly	Ala	Met	Asn	His	Asp	Thr	Asn	Tyr	Ser	Phe	Gln
275				280				285							
Val	Gln	Cys	Gly	Leu	Ile	Val	Val	Ala	Tyr	Lys	Asp	Gly	Ser	Pro	Ala
290				295				300							
His	Pro	His	Leu	Met	Asp	Ala	Glu	Leu	Cys	Ser	Gln	Tyr	Trp	Thr	Lys
305				310				315							
Trp	Leu	Leu	Arg	Leu	Glu	Glu	Tyr	Thr	Glu	Lys	Lys	Lys	Asn	Gln	Asn
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340															

<210> 70
 <211> 1998
 <212> DNA
 <213> Homo sapiens

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ctttttgaaa	taagtgcaga	tatttattta	accctccctt	ccccaccctc	tgccccactt	360	
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80/175

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gtgatatcct tatttgctag cagaaaaggg actaacgtcc cattcctctt ttctgtgcg 660
tccactggct agagagcagg cgggtgcgcgg ttgggcagac acctgggagg agtctccaag 720
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ccacatcccc taacatctga ttacgactt aatgtatgtt gtaagaaaag aaaaaagaaa 1920
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<210> 71

<211> 1763

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (540).. (1529)

<400> 71

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aagtccatgt ggctcttcac agtgaatcag gtgttaagga agatgcagag acgccacagc 240
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81/175

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<210> 72

<211> 330

<212> PRT

<213> Homo sapiens

<400> 72

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          20           25           30
Gly Gly Ser Leu Leu Gln His Val Gly Gly Asp His Arg Gly His Ser
          35           40           45
Glu Glu Gly Gly Asp Glu Gln Pro Gly Thr Pro Ala Pro Ala Leu Ser
          50           55           60
Glu Leu Lys Ala Val Ile Cys Trp Leu Gln Lys Gly Leu Pro Phe Ile
          65           70           75           80
Leu Ile Leu Leu Ala Lys Leu Cys Phe Gln His Lys Leu Gly Ile Ala
          85           90           95
Val Cys Ile Gly Met Ala Ser Thr Phe Ala Tyr Ala Asn Ser Thr Leu
          100          105          110
Arg Glu Gln Val Ser Leu Lys Glu Lys Arg Ser Val Leu Val Ile Leu
          115          120          125
Trp Ile L u Ala Phe Leu Ala Gly Asn Thr Leu Tyr Val Leu Tyr Thr
          130          135          140
Phe Ser S r Gln Gln Leu Tyr Asn Ser Leu Ile Phe Leu Lys Pro Asn

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82/175

145					150					155				160	
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				165					170					175	
Asp	Phe	Val	Leu	Lys	Tyr	Ile	Thr	Ile	Ala	Leu	Lys	Cys	Leu	Ile	Val
			180					185					190		
Ala	Leu	Pro	Lys	Ile	Ile	Leu	Ala	Val	Lys	Ser	Lys	Gly	Lys	Phe	Tyr
		195				200						205			
Leu	Val	Ile	Glu	Glu	Leu	Ser	Gln	Leu	Phe	Arg	Ser	Leu	Val	Pro	Ile
	210				215					220					
Gln	Leu	Trp	Tyr	Lys	Tyr	Ile	Met	Gly	Asp	Asp	Ser	Ser	Asn	Ser	Tyr
225					230				235						240
Phe	Leu	Gly	Gly	Val	Leu	Ile	Val	Leu	Tyr	Ser	Leu	Cys	Lys	Ser	Phe
				245				250						255	
Asp	Ile	Cys	Gly	Arg	Val	Gly	Gly	Val	Arg	Lys	Ala	Leu	Lys	Leu	Leu
			260					265					270		
Cys	Thr	Ser	Gln	Asn	Tyr	Gly	Val	Arg	Ala	Thr	Gly	Gln	Gln	Cys	Thr
		275				280						285			
Glu	Ala	Gly	Asp	Ile	Cys	Ala	Ile	Cys	Gln	Ala	Glu	Phe	Arg	Glu	Pro
	290				295					300					
Leu	Ile	Leu	Leu	Cys	Gln	Met	Leu	Leu	Lys	Gly	His	Lys	Lys	Leu	Glu
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Leu	Glu	Lys	Ile	Asp	Glu	Ser	Ala	Gly	Val						
				325				330							

<210> 73
 <211> 3493
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (40).. (396)

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 aagttacttc totgatttcc agtttcctta tctgcaaaat ggagacctta gggagttaat 720
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83/175

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84/175

<210> 74
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 74
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 35 40 45
 Cys Tyr Ser Leu Leu Gly Met Glu Arg Ser Gly Thr Ala Val Gln Arg
 50 55 60
 Ser Trp Pro Arg Arg Ser Ser Gly Ile Pro Val Pro Arg Ala Val His
 65 70 75 80
 Ser Val Ile Leu Arg Leu Pro Gly Val Glu Gly Ile Thr Cys Trp Val
 85 90 95
 Leu Glu Ser Ile Ala Leu His Leu Arg Lys Glu Lys Ser Gln Lys Asp
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 Lys Met Thr Cys Pro Arg Ser
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 <213> Homo sapiens

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 <222> (98).. (1027)

<400> 75
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85/175

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<210> 76

<211> 310

<212> PRT

<213> Homo sapiens

<400> 76

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      20             25            30
Leu Asn Val Gly Gly Ala Leu Tyr Tyr Thr Thr Met Gln Thr Leu Thr
      35             40            45
Lys Gln Asp Thr Met Leu Lys Ala Met Phe Ser Gly Arg Met Glu Val
      50             55            60
Leu Thr Asp Ser Glu Gly Trp Ile Leu Ile Asp Arg Cys Gly Lys His

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86/175

65					70						75					80
Phe	Gly	Thr	Ile	Leu	Asn	Tyr	Leu	Arg	Asp	Gly	Ala	Val	Pro	Leu	Pro	
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Glu	Ser	Arg	Arg	Glu	Ile	Glu	Glu	Leu	Leu	Ala	Glu	Ala	Lys	Tyr	Tyr	
			100					105					110			
Leu	Val	Gln	Gly	Leu	Val	Glu	Glu	Cys	Gln	Ala	Ala	Leu	Gln	Asn	Lys	
		115					120					125				
Asp	Thr	Tyr	Glu	Pro	Phe	Cys	Lys	Val	Pro	Val	Ile	Thr	Ser	Ser	Lys	
	130					135					140					
Glu	Glu	Gln	Lys	Leu	Ile	Ala	Thr	Ser	Asn	Lys	Pro	Ala	Val	Lys	Leu	
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Leu	Tyr	Asn	Arg	Ser	Asn	Asn	Lys	Tyr	Ser	Tyr	Thr	Ser	Asn	Ser	Asp	
				165					170					175		
Asp	Asn	Met	Leu	Lys	Asn	Ile	Glu	Leu	Phe	Asp	Lys	Leu	Ser	Leu	Arg	
			180					185					190			
Phe	Asn	Gly	Arg	Val	Leu	Phe	Ile	Lys	Asp	Val	Ile	Gly	Asp	Glu	Ile	
		195					200					205				
Cys	Cys	Trp	Ser	Phe	Tyr	Gly	Gln	Gly	Arg	Lys	Ile	Ala	Glu	Val	Cys	
	210					215					220					
Cys	Thr	Ser	Ile	Val	Tyr	Ala	Thr	Glu	Lys	Lys	Gln	Thr	Lys	Val	Glu	
225					230					235					240	
Phe	Pro	Glu	Ala	Arg	Ile	Tyr	Glu	Glu	Thr	Leu	Asn	Ile	Leu	Leu	Tyr	
				245					250						255	
Glu	Ala	Gln	Asp	Gly	Arg	Gly	Pro	Asp	Asn	Ala	Leu	Leu	Glu	Ala	Thr	
			260					265					270			
Gly	Gly	Ala	Ala	Gly	Arg	Ser	His	His	Leu	Asp	Glu	Asp	Glu	Glu	Arg	
		275					280					285				
Glu	Arg	Ile	Glu	Arg	Val	Arg	Arg	Ile	His	Ile	Lys	Arg	Pro	Asp	Asp	
	290					295					300					
Arg	Ala	His	Leu	His	Gln											
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<210> 77

<211> 2517

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (274).. (687)

<400> 77

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tctgtctga gccccaaaggc acctcagggt caagagcaac agggccaaga ggatgaagtg 180
gtcttggtgg aagggccac cctccagag acccccgcac tcttccact caaatccgt 240
tgccgggctg acctggtcag attgccctc aggatgtcgg agcccctgca gagtgtggtg 300

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87/175

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gactgtgtgg tactaacaag ttctccagag gccacagaga cgtcccaaca gctccagctc 480
cgggtgcagg gaaaggagaa acaccagaca ctggaagtct cactgtctcg agattccctt 540
ctaaagacco ttatgtccca ctatgaggag gccatgggac tgtcgggacg gaagctctcc 600
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<210> 78

<211> 138

<212> PRT

<213> Homo sapiens

<400> 78

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Gly Val Ser Pro Ser Arg Ile Leu Leu Leu Phe Gly Glu Thr Glu Leu

88/175

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		35					40					45					
Ile	Asp	Cys	Val	Val	Leu	Thr	Ser	Ser	Pro	Glu	Ala	Thr	Glu	Thr	Ser		
	50					55					60						
Gln	Gln	Leu	Gln	Leu	Arg	Val	Gln	Gly	Lys	Glu	Lys	His	Gln	Thr	Leu		
65					70					75					80		
Glu	Val	Ser	Leu	Ser	Arg	Asp	Ser	Pro	Leu	Lys	Thr	Leu	Met	Ser	His		
				85				90						95			
Tyr	Glu	Glu	Ala	Met	Gly	Leu	Ser	Gly	Arg	Lys	Leu	Ser	Phe	Phe	Phe		
			100				105						110				
Asp	Gly	Thr	Lys	Leu	Ser	Gly	Arg	Glu	Leu	Pro	Ala	Asp	Leu	Gly	Met		
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<210> 79

<211> 2901

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91).. (1974)

<400> 79

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89/175

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<210> 80

<211> 628

<212> PRT

<213> Homo sapiens

<400> 80

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Arg Lys His Glu Leu Leu Ala Lys Ala Leu His Leu Leu Lys Ser Ser
      35           40           45
Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu Leu Tyr Arg Arg Arg
      50           55           60
Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu
      65           70           75           80
Pro Pro Gly Thr Ser Pro Val Gly Ser Pro Gly Pro Leu Ala Pro Ile
      85           90           95

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90/175

Pro Pro Thr Leu Leu Ala Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu
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 Val Asp Met His Pro Pro Leu Pro Gln Pro Val His Pro Asp Val Thr
 115 120 125
 Met Lys Pro Leu Pro Phe Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro
 130 135 140
 Thr Thr Leu Ala Ser Thr Ser Ser Gln Arg Phe Glu Glu Ala His Phe
 145 150 155 160
 Thr Phe Ala Leu Thr Pro Gln Gln Val Gln Ile Leu Thr Ser Arg
 165 170 175
 Glu Val Leu Pro Gly Ala Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu
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 Tyr Leu Pro Pro Thr Lys Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg
 225 230 235 240
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 260 265 270
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 275 280 285
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 Lys Glu Lys Leu Thr Ala Asp Pro Asp Ser Glu Val Ala Thr Thr Ser
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 Glu Asp Gly Ser Trp Cys Pro Met Lys Pro Lys Lys Glu Ala Ser Glu
 405 410 415
 Val Cys Pro Pro Pro Gly Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro
 420 425 430
 Val Gln Gly Gly Asp Pro Ser Glu Asn Lys Lys Lys Val Glu Val Ile
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 Asp Leu Thr Ile Glu Ser Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr
 450 455 460
 Lys Lys His Cys Ser Val Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly
 465 470 475 480

91/175

Ser Lys Gly Val Leu Thr Ser Gly His Gln Pro Ser Ser Val Leu Arg
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 Ser Pro Ala Met Gly Thr Leu Gly Gly Asp Phe Leu Ser Ser Leu Pro
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 515 520 525
 Leu Asp Leu Phe Ser Phe Leu Gln Thr Glu Ser Gln His Tyr Gly Pro
 530 535 540
 Ser Val Ile Thr Ser Leu Asp Glu Gln Asp Ala Leu Gly His Phe Phe
 545 550 555 560
 Gln Tyr Arg Gly Thr Pro Ser His Phe Leu Gly Pro Leu Ala Pro Thr
 565 570 575
 Leu Gly Ser Ser His Cys Ser Ala Thr Pro Ala Pro Pro Pro Gly Arg
 580 585 590
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 610 615 620
 Ile Ser Leu Asp
 625

<210> 81

<211> 2130

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (186).. (1262)

<400> 81

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92/175

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<210> 82

<211> 359

<212> PRT

<213> Homo sapiens

<400> 82

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          20             25             30
Thr Val Pro Glu Cys Ala Ile Cys Leu Gln Thr Cys Val His Pro Val
          35             40             45
Ser Leu Pro Cys Lys His Val Phe Cys Tyr Leu Cys Val Lys Gly Ala
          50             55             60
Ser Trp Leu Gly Lys Arg Cys Ala Leu Cys Arg Gln Glu Ile Pro Glu
          65             70             75             80
Asp Phe Leu Asp Lys Pro Thr Leu Leu Ser Pro Glu Glu Leu Lys Ala
          85             90             95
Ala Ser Arg Gly Asn Gly Glu Tyr Ala Trp Tyr Tyr Glu Gly Arg Asn
          100            105            110
Gly Trp Trp Gln Tyr Asp Glu Arg Thr Ser Arg Glu Leu Glu Asp Ala
          115            120            125
Phe S r Lys Gly Lys Lys Asn Thr Glu Met Leu Ile Ala Gly Phe Leu
          130            135            140
Tyr Val Ala Asp Leu Glu Asn Met Val Gln Tyr Arg Arg Asn Glu His
          145            150            155            160

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93/175

Gly Arg Arg Arg Lys Ile Lys Arg Asp Ile Ile Asp Ile Pro Lys Lys
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 Gly Val Ala Gly Leu Arg Leu Asp Cys Asp Ala Asn Thr Val Asn Leu
 180 185 190
 Ala Arg Glu Ser Ser Ala Asp Gly Ala Asp Ser Val Ser Ala Gln Ser
 195 200 205
 Gly Ala Ser Val Gln Pro Leu Val Ser Ser Val Arg Pro Leu Thr Ser
 210 215 220
 Val Asp Gly Gln Leu Thr Ser Pro Ala Thr Pro Ser Pro Asp Ala Ser
 225 230 235 240
 Thr Ser Leu Glu Asp Ser Phe Ala His Leu Gln Leu Ser Gly Asp Asn
 245 250 255
 Thr Ala Glu Arg Ser His Arg Gly Glu Gly Glu Glu Asp His Glu Ser
 260 265 270
 Pro Ser Ser Gly Arg Val Pro Ala Pro Asp Thr Ser Ile Glu Glu Thr
 275 280 285
 Glu Ser Asp Ala Ser Ser Asp Ser Glu Asp Val Ser Ala Val Val Ala
 290 295 300
 Gln His Ser Leu Thr Gln Gln Arg Leu Leu Val Ser Asn Ala Asn Gln
 305 310 315 320
 Thr Val Pro Asp Arg Ser Asp Arg Ser Gly Thr Asp Arg Ser Val Ala
 325 330 335
 Gly Gly Gly Thr Val Ser Val Ser Val Arg Ser Arg Arg Pro Asp Gly
 340 345 350
 Gln Cys Thr Val Thr Glu Val
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<210> 83

<211> 2748

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (250).. (1011)

<400> 83

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 gaagcacaag gaaaaattga tgtacttcaa gctgaagtag ctgcattgaa gacacttgta 360
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 aaaaaggggc atacaagaaa taaaagcaca agcagtgcta tgagtggcag tcatcaggac 480
 ctcagtgatg tacagccaat tgtaaaagac tgcaaagagg ctgacttatc cttgtataat 540
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94/175

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cggtttgtga aagcttctgc agttgaatgc ggaggaccaa aaaaatgtgc tctcactggc 780
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<210> 84

<211> 254

<212> PRT

<213> Homo sapiens

<400> 84

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          20          25          30

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95/175

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Leu Lys Thr Leu Val Leu Ser Ser Ser Pro Thr Ser Pro Thr Gln Glu
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Pro Leu Pro Gly Gly Lys Thr Pro Phe Lys Lys Gly His Thr Arg Asn
      50              55              60
Lys Ser Thr Ser Ser Ala Met Ser Gly Ser His Gln Asp Leu Ser Val
      65              70              75              80
Ile Gln Pro Ile Val Lys Asp Cys Lys Glu Ala Asp Leu Ser Leu Tyr
      85              90              95
Asn Glu Phe Arg Leu Trp Lys Asp Glu Pro Thr Met Asp Arg Thr Cys
      100             105             110
Pro Phe Leu Asp Lys Ile Tyr Gln Glu Asp Ile Phe Pro Cys Leu Thr
      115             120             125
Phe Ser Lys Ser Glu Leu Ala Ser Ala Val Leu Glu Ala Val Glu Asn
      130             135             140
Asn Thr Leu Ser Ile Glu Pro Val Gly Leu Gln Pro Ile Arg Phe Val
      145             150             155             160
Lys Ala Ser Ala Val Glu Cys Gly Gly Pro Lys Lys Cys Ala Leu Thr
      165             170             175
Gly Gln Ser Lys Ser Cys Lys His Arg Ile Lys Leu Gly Asp Ser Ser
      180             185             190
Asn Tyr Tyr Tyr Ile Ser Pro Phe Cys Arg Tyr Arg Ile Thr Ser Val
      195             200             205
Cys Asn Phe Phe Thr Tyr Ile Arg Tyr Ile Gln Gln Gly Leu Val Lys
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Gln Gln Asp Val Asp Gln Met Phe Trp Glu Val Met Gln Leu Arg Lys
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<211> 2944

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (265).. (2031)

<400> 85

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cccgagaata gtcctgtcca gcagtttaag gaagaaatct ctaaactgtt taaatcacat 480

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96/175

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<210> 86

<211> 589

<212> PRT

<213> Homo sapiens

97/175

<400> 86

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Glu	Pro	Lys	Ile	Met	Lys	Val	Thr	Val	Lys	Thr	Pro	Lys	Glu	Lys	Glu	35	40	45	
Glu	Phe	Ala	Val	Pro	Glu	Asn	Ser	Ser	Val	Gln	Gln	Phe	Lys	Glu	Glu	50	55	60	
Ile	Ser	Lys	Arg	Phe	Lys	Ser	His	Thr	Asp	Gln	Leu	Val	Leu	Ile	Phe	65	70	75	80
Ala	Gly	Lys	Ile	Leu	Lys	Asp	Gln	Asp	Thr	Leu	Ser	Gln	His	Gly	Ile	85	90	95	
His	Asp	Gly	Leu	Thr	Val	His	Leu	Val	Ile	Lys	Thr	Gln	Asn	Arg	Pro	100	105	110	
Gln	Asp	His	Ser	Ala	Gln	Gln	Thr	Asn	Thr	Ala	Gly	Ser	Asn	Val	Thr	115	120	125	
Thr	Ser	Ser	Thr	Pro	Asn	Ser	Asn	Ser	Thr	Ser	Gly	Ser	Ala	Thr	Ser	130	135	140	
Asn	Pro	Phe	Gly	Leu	Gly	Gly	Leu	Gly	Gly	Leu	Ala	Gly	Leu	Ser	Ser	145	150	155	160
Leu	Gly	Leu	Asn	Thr	Thr	Asn	Phe	Ser	Glu	Leu	Gln	Ser	Gln	Met	Gln	165	170	175	
Arg	Gln	Leu	Leu	Ser	Asn	Pro	Glu	Met	Met	Val	Gln	Ile	Met	Glu	Asn	180	185	190	
Pro	Phe	Val	Gln	Ser	Met	Leu	Ser	Asn	Pro	Asp	Leu	Met	Arg	Gln	Leu	195	200	205	
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Ile	Ser	His	Met	Leu	Asn	Asn	Pro	Asp	Ile	Met	Arg	Gln	Thr	Leu	Glu	225	230	235	240
Leu	Ala	Arg	Asn	Pro	Ala	Met	Met	Gln	Glu	Met	Met	Arg	Asn	Gln	Asp	245	250	255	
Arg	Ala	Leu	Ser	Asn	Leu	Glu	Ser	Ile	Pro	Gly	Gly	Tyr	Asn	Ala	Leu	260	265	270	
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Glu	Gln	Phe	Gly	Gly	Asn	Pro	Phe	Ala	Ser	Leu	Val	Ser	Asn	Thr	Ser	290	295	300	
Ser	Gly	Glu	Gly	Ser	Gln	Pro	Ser	Arg	Thr	Glu	Asn	Arg	Asp	Pro	Leu	305	310	315	320
Pro	Asn	Pro	Trp	Ala	Pro	Gln	Thr	Ser	Gln	Ser	Ser	Ser	Ala	Ser	Ser	325	330	335	
Gly	Thr	Ala	Ser	Thr	Val	Gly	Gly	Thr	Thr	Gly	Ser	Thr	Ala	Ser	Gly	340	345	350	
Thr	Ser	Gly	Gln	Ser	Thr	Thr	Ala	Pro	Asn	Leu	Val	Pro	Gly	Val	Gly	355	360	365	

98/175

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 Thr Glu Asn Pro Gln Leu Met Gln Asn Met Leu Ser Ala Pro Tyr Met
 385 390 395 400
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 405 410 415
 Met Met Leu Asn Asn Pro Leu Phe Ala Gly Asn Pro Gln Leu Gln Glu
 420 425 430
 Gln Met Arg Gln Gln Leu Pro Thr Phe Leu Gln Gln Met Arg Asn Pro
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 Asp Thr Leu Ser Ala Met Ser Asn Pro Arg Ala Met Gln Ala Leu Leu
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 Ile Pro Gly Phe Thr Pro Gly Leu Gly Ala Leu Gly Ser Thr Gly Gly
 485 490 495
 Ser Ser Gly Thr Asn Gly Ser Asn Ala Thr Pro Ser Glu Asn Thr Ser
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 Pro Thr Ala Gly Thr Thr Glu Pro Gly His Gln Gln Phe Ile Gln Gln
 515 520 525
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 Val Arg Phe Gln Gln Gln Leu Glu Gln Leu Ser Ala Met Gly Phe Leu
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<210> 87

<211> 2160

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (197).. (496)

<400> 87

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99/175

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cacctcaatt tattttataa attcgttcat ttttctgtt atgttttata taatatatgg 2100
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<210> 88

<211> 100

<212> PRT

<213> Homo sapiens

<400> 88

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Gln Ala Ser Leu Ser Ala Asn Thr Phe Ala Ile Thr Gly His Ala Glu
      20             25             30
Ala Lys Pro Ile Thr Glu Met Leu Pro Gly Ile Leu Ser Gln Leu Gly
      35             40             45
Ala Asp Ser Leu Thr Ser Leu Arg Lys Leu Ala Glu Gln Phe Pro Arg
      50             55             60
Gln Val Leu Asp Ser Lys Ala Pro Lys Pro Glu Asp Ile Asp Glu Glu
      65             70             75             80
Asp Asp Asp Val Pro Asp L u Val Glu Asn Phe Asp Glu Ala Ser Lys
      85             90             95

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Asn Glu Ala Asn
100

<210> 89
<211> 2551
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (42)..(1883)

<400> 89
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<210> 90

<211> 614

<212> PRT

<213> Homo sapiens

<400> 90

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          20           25           30
Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg Glu Leu Pro
        35           40           45
Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn Tyr Arg Asp
        50           55           60
Met Gly Glu His Arg Val Ile Leu Pro Asp Asp Val Arg Asp Phe Ile
        65           70           75           80
Asp Asn Leu Asp Arg Pro Pro Gly Ser Ser Tyr Phe Arg Tyr Ala Glu
          85           90           95
Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu His Lys Phe Phe
        100          105          110
Asn Ile Pro Phe Leu Gln Leu Gln Arg Glu Thr Leu Leu Arg Gln Leu
        115          120          125
Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu Glu Leu Ser Val
        130          135          140
Gln Gln Glu Thr Glu Asp Gln Asn Tyr Gly Ile Phe Leu Glu Met Met
        145          150          155          160
Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala Ala Asn Gly Gln
          165          170          175
Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Val Pro Ala Gly Ala Val
        180          185          190
Ser Thr Gly Ser Ser Ser Pro Gly Thr Pro Gln Pro Ala Pro Gln Leu
        195          200          205
Pro Leu Asn Ala Ala Pro Pro Ser Ser Val Pro Pro Val Pro Pro Ser
        210          215          220
Glu Ala Leu Pro Pro Pro Ala Cys Pro Ser Ala Pro Ala Pro Arg Arg
        225          230          235          240
Ser Ile Ile Ser Arg Leu Phe Gly Thr Ser Pro Ala Thr Glu Ala Ala

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245														250				255	
Pro	Pro	Pro	Pro	Glu	Pro	Val	Pro	Ala	Ala	Gln	Gly	Pro	Ala	Thr	Val				
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Gln	Ser	Val	Glu	Asp	Phe	Val	Pro	Asp	Asp	Arg	Leu	Asp	Arg	Ser	Phe				
275				Thr	Thr	Pro	Ala	Arg	Asp	Glu	Lys	Lys	Val	Gly	Ala				
Leu	Glu	Asp	Thr	Thr	Pro	Ala	Arg	Asp	Glu	Lys	Lys	Val	Gly	Ala	Lys				
290				Asp	Thr	Pro	Ala	Arg	Asp	Glu	Lys	Lys	Val	Gly	Ala				
Ala	Ala	Gln	Gln	Asp	Ser	Asp	Ser	Asp	Gly	Glu	Ala	Leu	Gly	Gly	Asn				
305				Asp	Ser	Asp	Ser	Asp	Gly	Glu	Ala	Leu	Gly	Gly	Asn				
Pro	Met	Val	Ala	Gly	Phe	Gln	Asp	Asp	Val	Asp	Leu	Glu	Asp	Gln	Pro				
325				Pro	Leu	Pro	Ala	Gly	Pro	Val	Pro	Ser	Gln	Asp	Ile				
Arg	Gly	Ser	Pro	Pro	Leu	Pro	Ala	Gly	Pro	Val	Pro	Ser	Gln	Asp	Ile				
340				Pro	Leu	Pro	Ala	Gly	Pro	Val	Pro	Ser	Gln	Asp	Ile				
Thr	Leu	Ser	Ser	Glu	Glu	Glu	Ala	Glu	Val	Ala	Ala	Pro	Thr	Lys	Gly				
355				Glu	Glu	Glu	Ala	Glu	Val	Ala	Ala	Pro	Thr	Lys	Gly				
Pro	Ala	Pro	Ala	Pro	Gln	Gln	Cys	Ser	Glu	Pro	Glu	Thr	Lys	Trp	Ser				
370				Pro	Gln	Gln	Cys	Ser	Glu	Pro	Glu	Thr	Lys	Trp	Ser				
Ser	Ile	Pro	Ala	Ser	Lys	Pro	Arg	Arg	Gly	Thr	Ala	Pro	Thr	Arg	Thr				
385				Ser	Lys	Pro	Arg	Arg	Gly	Thr	Ala	Pro	Thr	Arg	Thr				
Ala	Ala	Pro	Pro	Trp	Pro	Gly	Gly	Val	Ser	Val	Arg	Thr	Gly	Pro	Glu				
405				Pro	Gly	Gly	Val	Ser	Val	Arg	Thr	Gly	Pro	Glu					
Lys	Arg	Ser	Ser	Thr	Arg	Pro	Pro	Ala	Glu	Met	Glu	Pro	Gly	Lys	Gly				
420				Thr	Arg	Pro	Pro	Ala	Glu	Met	Glu	Pro	Gly	Lys	Gly				
Glu	Gln	Ala	Ser	Ser	Ser	Glu	Ser	Asp	Pro	Glu	Gly	Pro	Ile	Ala	Ala				
435				Ser	Ser	Glu	Ser	Asp	Pro	Glu	Gly	Pro	Ile	Ala	Ala				
Gln	Met	Leu	Ser	Phe	Val	Met	Asp	Asp	Pro	Asp	Phe	Glu	Ser	Glu	Gly				
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Ser	Asp	Thr	Gln	Arg	Arg	Ala	Asp	Asp	Phe	Pro	Val	Arg	Asp	Asp	Pro				
465				Arg	Arg	Ala	Asp	Asp	Phe	Pro	Val	Arg	Asp	Asp	Pro				
Ser	Asp	Val	Thr	Asp	Glu	Asp	Glu	Gly	Pro	Ala	Glu	Pro	Pro	Pro	Pro				
485				Asp	Glu	Asp	Glu	Gly	Pro	Ala	Glu	Pro	Pro	Pro	Pro				
Pro	Lys	Leu	Pro	Leu	Pro	Ala	Phe	Arg	Leu	Lys	Asn	Asp	Ser	Asp	Leu				
500				Leu	Pro	Ala	Phe	Arg	Leu	Lys	Asn	Asp	Ser	Asp	Leu				
Phe	Gly	Leu	Gly	Leu	Glu	Glu	Ala	Gly	Pro	Lys	Glu	Ser	Ser	Glu	Glu				
515				Leu	Glu	Glu	Ala	Gly	Pro	Lys	Glu	Ser	Ser	Glu	Glu				
Gly	Lys	Glu	Gly	Lys	Thr	Pro	Ser	Lys	Glu	Lys	Lys	Lys	Lys	Lys	Lys				
530				Lys	Thr	Pro	Ser	Lys	Glu	Lys	Lys	Lys	Lys	Lys	Lys				
Lys	Gly	Lys	Glu	Glu	Glu	Glu	Lys	Ala	Ala	Lys	Lys	Lys	Ser	Lys	His				
545				Glu	Glu	Glu	Lys	Ala	Ala	Lys	Lys	Lys	Ser	Lys	His				
Lys	Lys	Ser	Lys	Asp	Lys	Glu	Glu	Gly	Lys	Glu	Glu	Arg	Arg	Arg	Arg				
565				Asp	Lys	Glu	Glu	Gly	Lys	Glu	Glu	Arg	Arg	Arg	Arg				
Gln	Gln	Arg	Pro	Pro	Arg	Ser	Arg	Glu	Arg	Thr	Ala	Ala	Asp	Glu	Leu				
580				Pro	Arg	Ser	Arg	Glu	Arg	Thr	Ala	Ala	Asp	Glu	Leu</				

103/175

<210> 91
<211> 3133
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (113).. (1879)

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ctacaatgct gccagcttat ttggattccc attccagctg accacaaago ccatggtaac 360
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tcctaattgga ataagtgact atccaaagat cagagtgaac gttacccgag atcagccacg 540
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ggctgttaaca gagatgattt ctgaagagag tggcaagggt ctgaggcgctc ccctattgtac 720
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104/175

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<210> 92

<211> 589

<212> PRT

<213> Homo sapiens

<400> 92

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      20             25             30
Asp Ser Thr Leu Phe Ser Thr Val Asp Thr Asp Glu Ile Pro Ala Lys
      35             40             45
Arg Pro Arg Leu Asp Cys Phe Ile His Gln Val Lys Asn Ser Leu Tyr
      50             55             60
Asn Ala Ala Ser Leu Phe Gly Phe Pro Phe Gln Leu Thr Thr Lys Pro
      65             70             75             80
Met Val Thr Ser Ala Cys Asn Gly Thr Arg Asn Val Ala Pro Ser Gly
      85             90             95
Glu Val Phe Ser Asn Ser Ser Ser Cys Glu Leu Thr Gly Ser Gly Ser
      100            105            110
Trp Asn Asn Met Leu Lys Leu Gly Asn Lys Ser Pro Asn Gly Ile Ser
      115            120            125
Asp Tyr Pro Lys Ile Arg Val Thr Val Thr Arg Asp Gln Pro Arg Arg
      130            135            140
Val Leu Pro Ser Phe Gly Phe Thr Leu Asn Ser Glu Gly Cys Asn Arg
      145            150            155            160
Arg Pro Gly Gly Arg Arg His Ser Lys Gly Asn Pro Glu Ser Ser Leu
      165            170            175
Met Trp Lys Pro Gln Glu Gln Ala Val Thr Glu Met Ile Ser Glu Glu
      180            185            190

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105/175

Ser Gly Lys Gly Leu Arg Arg Pro His Cys Thr Val Glu Glu Gly Val
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 Gln Lys Glu Glu Arg Glu Lys Tyr Arg Lys Leu Leu Glu Arg Leu Lys
 210 215 220
 Glu Ser Gly His Gly Asn Ser Val Cys Pro Val Thr Ser Asn Tyr His
 225 230 235 240
 Ser Ser Gln Arg Ser Gln Met Asp Thr Leu Lys Thr Lys Gly Trp Gly
 245 250 255
 Glu Glu Gln Asn His Gly Val Lys Thr Thr Gln Phe Val Pro Lys Gln
 260 265 270
 Tyr Arg Leu Val Glu Thr Arg Gly Pro Leu Cys Ser Leu Arg Ser Glu
 275 280 285
 Lys Arg Cys Ser Lys Gly Lys Ile Thr Asp Thr Glu Lys Met Val Gly
 290 295 300
 Ile Arg Phe Glu Asn Glu Ser Arg Arg Gly Tyr Gln Leu Glu Pro Asp
 305 310 315 320
 Leu Ser Glu Glu Val Ser Ala Arg Leu Arg Gly Ser Gly Ser Asn
 325 330 335
 Gly Leu Leu Arg Arg Lys Val Ser Ile Glu Thr Lys Glu Lys Asn
 340 345 350
 Cys Ser Gly Lys Glu Arg Asp Arg Thr Asp Asp Leu Glu Leu
 355 360 365
 Thr Glu Asp Met Glu Lys Glu Ile Ser Asn Ala Leu Gly His Gly Pro
 370 375 380
 Gln Asp Glu Ile Leu Ser Ser Ala Phe Lys Leu Arg Ile Thr Arg Gly
 385 390 395 400
 Asp Ile His Thr Leu Lys Asn Tyr His Trp Leu Asn Asp Glu Val Ile
 405 410 415
 Asn Phe Tyr Met Asn Leu Leu Val Glu Arg Asn Lys Lys Gln Gly Tyr
 420 425 430
 Pro Ala Leu His Val Phe Ser Thr Phe Phe Tyr Pro Lys Leu Lys Ser
 435 440 445
 Gly Gly Tyr Gln Ala Val Lys Arg Trp Thr Lys Gly Val Asn Leu Phe
 450 455 460
 Glu Gln Glu Ile Ile Leu Val Pro Ile His Arg Lys Val His Trp Ser
 465 470 475 480
 Leu Val Val Ile Asp Leu Arg Lys Lys Cys Leu Lys Tyr Leu Asp Ser
 485 490 495
 Met Gly Gln Lys Gly His Arg Ile Cys Glu Ile Leu Leu Gln Tyr Leu
 500 505 510
 Gln Asp Glu Ser Lys Thr Lys Arg Asn Ser Asp Leu Asn Leu Leu Glu
 515 520 525
 Trp Thr His His Ser Met Lys Pro His Glu Ile Pro Gln Gln Leu Asn
 530 535 540
 Gly Ser Asp Cys Gly Met Phe Thr Cys Lys Tyr Ala Asp Tyr Ile Ser
 545 550 555 560
 Arg Asp Lys Pro Ile Thr Phe Thr Gln His Gln Met Pro Leu Phe Arg
 565 570 575



106/175

Lys Lys Met Val Trp Glu Ile Leu His Gln Gln Leu Leu
580 585

<210> 93
<211> 2987
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (145)..(1926)

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cacgtgcaga ctcagatgtc actgatgaat gacttgactt caaagaacat ccctaattgga 240
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<210> 94

<211> 594

<212> PRT

<213> Homo sapiens

<400> 94

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      20             25             30
Ile Pro Ala Val Pro Cys His Ala Pro Ser His Ser Glu Ser Gln Ala
      35             40             45
Thr Pro His Ser Ser Tyr Gly Leu Cys Thr Ser Thr Pro Val Trp Ser
      50             55             60
Leu Gln Arg Pro Pro Cys Pro Pro Lys Val His Ser Glu Val Gln Thr
      65             70             75             80
Asp Gly Asn Ser Gln Phe Ala Ser Gln Glu Asp Ser Glu Ile Gln Arg
      85             90             95
Leu Ile Thr Glu Met Glu Ala Cys Ile Ser Val Leu Pro Thr Val Ser
      100            105            110
Gly Asn Thr Asp Ile Gln Val Glu Ile Ala Leu Ala Met Gln Pro Leu
      115            120            125
Arg Ser Glu Asn Ala Gln Leu Arg Arg Gln Leu Arg Ile Leu Asn Gln
      130            135            140
Gln Leu Arg Glu Gln Gln Lys Thr Gln Lys Pro Ser Gly Ala Val Asp
      145            150            155            160
Cys Asn Leu Glu Leu Phe Ser Leu Gln Ser Leu Asn Met Ser Leu Gln
      165            170            175
Asn Gln Leu Glu Ser Leu Lys Ser Gln Glu Leu Leu Gln Ser Lys
      180            185            190

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109/175

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 Glu Lys

<210> 95
 <211> 2534
 <212> DNA
 <213> Homo sapiens

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 <222> (84).. (1550)

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110/175

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<210> 96
 <211> 489
 <212> PRT
 <213> Homo sapiens

<400> 96

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          20           25           30
His Gly Glu Leu His Pro Ser Glu Gly Pro Trp Gly Ala Pro Arg Glu
        35           40           45
Asp Met Thr Pro Leu Asn Leu Ser Ser Arg Ala Glu Pro Val Arg Asp
        50           55           60
Ile Arg Cys Glu Phe Cys Gly Glu Phe Phe Glu Asn Arg Lys Gly Leu
        65           70           75           80
Ser Ser His Ala Arg Ser His Leu Arg Gln Met Gly Val Thr Glu Trp
          85           90           95
Ser Val Asn Gly Ser Pro Ile Asp Thr Leu Arg Glu Ile Leu Lys Lys
        100          105          110
Lys Ser Lys Pro Cys Leu Ile Lys Lys Glu Pro Pro Ala Gly Asp Leu
        115          120          125
Ala Pro Ala Leu Ala Glu Asp Gly Pro Pro Thr Val Ala Pro Gly Pro
        130          135          140
Val Gln Ser Pro Leu Pro Leu Ser Pro Leu Ala Gly Arg Pro Gly Lys
        145          150          155          160
Pro Gly Ala Gly Pro Ala Gln Val Pro Arg Glu Leu Ser Leu Thr Pro
          165          170          175
Ile Thr Gly Ala Lys Pro Ser Ala Thr Gly Tyr Leu Gly Ser Val Ala
          180          185          190
Ala Lys Arg Pro Leu Gln Glu Asp Arg Leu Leu Pro Ala Glu Val Lys
          195          200          205
Ala Lys Thr Tyr Ile Gln Thr Glu Leu Pro Phe Lys Ala Lys Thr Leu
          210          215          220
His Glu Lys Thr Ser His Ser Ser Thr Glu Ala Cys Cys Glu Leu Cys

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111/175

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Gly	Leu	Tyr	Phe	Glu	Asn	Arg	Lys	Ala	Leu	Ala	Ser	His	Ala	Arg Ala
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			260					265					270	
Ile	Glu	Thr	Leu	Ser	Glu	Trp	Ile	Lys	His	Arg	Pro	Gln	Lys	Val Gly
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Ala	Tyr	Arg	Ser	Tyr	Ile	Gln	Gly	Gly	Arg	Pro	Phe	Thr	Lys	Lys Phe
	290					295					300			
Arg	Ser	Ala	Gly	His	Gly	Arg	Asp	Ser	Asp	Lys	Arg	Pro	Ser	Leu Gly
305					310					315				320
Leu	Ala	Pro	Gly	Gly	Leu	Ala	Val	Val	Gly	Arg	Ser	Ala	Gly	Gly Glu
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Pro	Gly	Pro	Glu	Ala	Gly	Arg	Ala	Ala	Asp	Gly	Gly	Glu	Arg	Pro Leu
		340					345					350		
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	355					360					365			
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385					390				395					400
Glu	Val	Arg	Gln	Pro	Pro	Pro	Arg	Val	Arg	Pro	Val	Pro	Ser	Leu Val
			405					410					415	
Pro	Arg	Pro	Pro	Gln	Thr	Ser	Leu	Val	Lys	Phe	Val	Gly	Asn	Ile Tyr
		420					425					430		
Thr	Leu	Lys	Cys	Arg	Phe	Cys	Glu	Val	Glu	Phe	Gln	Gly	Pro	Leu Ser
	435					440					445			
Ile	Gln	Glu	Glu	Trp	Val	Arg	His	Leu	Gln	Arg	His	Ile	Leu	Glu Met
450					455				460					
Asn	Phe	Ser	Lys	Ala	Asp	Pro	Pro	Pro	Glu	Glu	Ser	Gln	Ala	Pro Gln
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Ala	Gln	Thr	Ala	Ala	Ala	Glu	Ala	Pro						
			485											

<210> 97

<211> 3741

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (110).. (892)

<400> 97

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112/175

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cccatttgca gtggttggca gcaccgaaga ggtgaagatt ggcaacaaga tggcaaaggc 360
caggcagtac ccttggggtg tgggtgcagg tgaagaatgaa aatcattgag attttgtgaa 420
acttcgagag atgctgatcc gctgaacat ggaggacttg cgagagcaga ctcacacccg 480
ccactatgaa ttgtaccgac gctgtaagct tgaagagatg gggttcaagg acactgaccc 540
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113/175

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<210> 98

<211> 261

<212> PRT

<213> Homo sapiens

<400> 98

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 20          25          30
Met Ser Glu Leu Val Ser Asn Gly Val Gln Ile Tyr Gln Phe Pro Thr
 35          40          45
Asp Glu Glu Thr Val Ala Glu Ile Asn Ala Thr Met Ser Val His Leu
 50          55          60
Pro Phe Ala Val Val Gly Ser Thr Glu Glu Val Lys Ile Gly Asn Lys
 65          70          75          80
Met Ala Lys Ala Arg Gln Tyr Pro Trp Gly Val Val Gln Val Glu Asn
 85          90          95
Glu Asn His Cys Asp Phe Val Lys Leu Arg Glu Met Leu Ile Arg Val
100          105          110
Asn Met Glu Asp Leu Arg Glu Gln Thr His Thr Arg His Tyr Glu Leu
115          120          125
Tyr Arg Arg Cys Lys Leu Glu Glu Met Gly Phe Lys Asp Thr Asp Pro
130          135          140
Asp Ser Lys Pro Phe Ser Leu Gln Glu Thr Tyr Glu Ala Lys Arg Asn
145          150          155          160
Glu Phe Leu Gly Glu Leu Gln Lys Lys Glu Glu Glu Met Arg Gln Met
165          170          175
Phe Val Met Arg Val Lys Glu Lys Glu Ala Glu Leu Lys Glu Ala Glu
180          185          190
Lys Glu Leu His Glu Lys Phe Asp Leu Leu Lys Arg Thr His Gln Glu
195          200          205
Glu Lys Lys Lys Val Glu Asp Lys Lys Lys Glu Leu Glu Glu Glu Val
210          215          220

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114/175

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 245 250 255
 Asn Ala Ser Phe Thr
 260

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 <211> 3389
 <212> DNA
 <213> Homo sapiens

<220>
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115/175

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<210> 100

<211> 463

<212> PRT

<213> Homo sapiens

<400> 100

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Asn Ser Thr Val Ala Leu Ala Lys Val Arg Ser Phe Gly Thr Glu Asp
  35             40             45
Arg Pro Thr Asp Arg Pro Ile Pro Pro Arg Asp Glu Val Phe Glu Tyr
  50             55             60
Ile Ile Phe Arg Gly Ser Asp Ile Lys Asp Leu Thr Val Cys Glu Pro
  65             70             75             80
Pro Lys Pro Gln Cys Ser Leu Pro Gln Asp Pro Ala Ile Val Gln Ser
  85             90             95
Ser Leu Gly Ser Ser Thr Ser Ser Phe Gln Ser Met Gly Ser Tyr Gly

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116/175

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Val	Gly	Gln	Gln	Phe	Gly	Ala	Val	Gly	Val	Ala	Gly	Ser	Ser	Leu	Thr
	130				135					140					
Ser	Phe	Gly	Thr	Glu	Thr	Ser	Asn	Ser	Gly	Thr	Leu	Pro	Gln	Ser	Ser
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Ala	Val	Gly	Ser	Ala	Phe	Thr	Gln	Asp	Thr	Arg	Ser	Leu	Lys	Thr	Gln
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Leu	Ser	Gln	Gly	Arg	Ser	Ser	Pro	Gln	Leu	Asp	Pro	Leu	Arg	Lys	Ser
		180						185					190		
Pro	Thr	Met	Glu	Gln	Ala	Val	Gln	Thr	Ala	Ser	Ala	His	Leu	Pro	Ala
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Ser	Ala	Ser	Gln	Lys	Ala	Gly	Glu	Asn	Gln	Glu	His	Arg	Gln	Ala	Glu
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Val	His	Lys	Val	Ser	Arg	Pro	Glu	Asn	Glu	Gln	Leu	Arg	Asn	Asp	Asn
				245				250						255	
Lys	Arg	Gln	Val	Ala	Pro	Gly	Ala	Pro	Ser	Ala	Pro	Arg	Arg	Gly	Arg
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Gly	Gly	His	Arg	Gly	Gly	Arg	Gly	Arg	Phe	Gly	Ile	Arg	Arg	Asp	Gly
		275					280					285			
Pro	Met	Lys	Phe	Glu	Lys	Asp	Phe	Asp	Phe	Glu	Ser	Ala	Asn	Ala	Gln
	290					295					300				
Phe	Asn	Lys	Glu	Glu	Ile	Asp	Arg	Glu	Phe	His	Asn	Lys	Leu	Lys	Leu
305					310					315					320
Lys	Glu	Asp	Lys	Leu	Glu	Lys	Gln	Glu	Lys	Pro	Val	Asn	Gly	Glu	Asp
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Lys	Gly	Asp	Ser	Gly	Val	Asp	Thr	Gln	Asn	Ser	Glu	Gly	Asn	Ala	Asp
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Glu	Glu	Asp	Pro	Leu	Gly	Pro	Asn	Cys	Tyr	Tyr	Asp	Lys	Thr	Lys	Ser
		355					360					365			
Phe	Phe	Asp	Asn	Ile	Ser	Cys	Asp	Asp	Asn	Arg	Glu	Arg	Arg	Pro	Thr
		370				375					380				
Trp	Ala	Glu	Glu	Arg	Arg	Leu	Asn	Ala	Glu	Thr	Phe	Gly	Ile	Pro	Leu
385					390					395					400
Arg	Pro	Asn	Arg	Gly	Arg	Gly	Gly	Tyr	Arg	Gly	Arg	Gly	Gly	Leu	Gly
				405					410					415	
Phe	Arg	Gly	Gly	Arg	Gly	Arg	Gly	Gly	Gly	Arg	Gly	Gly	Thr	Phe	Thr
			420					425					430		
Ala	Pro	Arg	Gly	Phe	Arg	Gly	Gly	Phe	Arg	Gly	Gly	Arg	Gly	Gly	Arg
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Glu	Phe	Ala	Asp	Phe	Glu	Tyr	Arg	Lys	Asp	Asn	Lys	Val	Ala	Ala	
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<210> 101

117/175

<211> 2284
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (128).. (1936)

<400> 101

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2284

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118/175

<210> 102
 <211> 603
 <212> PRT
 <213> Homo sapiens

<400> 102

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Arg Gly Arg Ser Phe Thr Ala Leu Arg Ser Ser Pro Leu Thr Val Thr
           35           40           45
Met Asp Trp Gln Ser Ile Lys Ile Gln Glu Leu Met Ser Asp Asp Gln
           50           55           60
Arg Glu Ala Gly Arg Ile Pro Arg Thr Ile Glu Cys Glu Leu Val His
           65           70           75           80
Asp Leu Val Asp Ser Cys Val Pro Gly Asp Thr Val Thr Ile Thr Gly
           85           90           95
Ile Val Lys Val Ser Asn Ala Glu Glu Gly Ser Arg Asn Lys Asn Asp
           100          105          110
Lys Cys Met Phe Leu Leu Tyr Ile Glu Ala Asn Ser Ile Ser Asn Ser
           115          120          125
Lys Gly Gln Lys Thr Lys Ser Ser Glu Asp Gly Cys Lys His Gly Met
           130          135          140
Leu Met Glu Phe Ser Leu Lys Asp Leu Tyr Ala Ile Gln Glu Ile Gln
           145          150          155          160
Ala Glu Glu Asn Leu Phe Lys Leu Ile Val Asn Ser Leu Cys Pro Val
           165          170          175
Ile Phe Gly His Glu Leu Val Lys Ala Gly Leu Ala Leu Ala Leu Phe
           180          185          190
Gly Gly Ser Gln Lys Tyr Ala Asp Asp Lys Asn Arg Ile Pro Ile Arg
           195          200          205
Gly Asp Pro His Ile Leu Val Val Gly Asp Pro Gly Leu Gly Lys Ser
           210          215          220
Gln Met Leu Gln Ala Ala Cys Asn Val Ala Pro Arg Gly Val Tyr Val
           225          230          235          240
Cys Gly Asn Thr Thr Thr Thr Ser Gly Leu Thr Val Thr Leu Ser Lys
           245          250          255
Asp Ser Ser Ser Gly Asp Phe Ala Leu Glu Ala Gly Ala Leu Val Leu
           260          265          270
Gly Asp Gln Gly Ile Cys Gly Ile Asp Glu Phe Asp Lys Met Gly Asn
           275          280          285
Gln His Gln Ala Leu Leu Glu Ala Met Glu Gln Gln Ser Ile Ser Leu
           290          295          300
Ala Lys Ala Gly Val Val Cys S r Leu Pro Ala Arg Thr S r Ile Ile
           305          310          315          320

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119/175

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Val 375	Phe 385	Ile 375	Leu 385	Leu 375	Asp 390	Thr 405	Pro 410	Asn 410	Glu 410	His 410	His 410	Asp 415	His 415	Leu 415	Leu 415	Val 415
Ser 370	Glu 385	His 370	Val 385	Ile 370	Ala 390	Ile 405	Arg 410	Ala 410	Gly 410	Lys 410	Gln 410	Arg 415	Thr 415	Ile 415	Ser 415	Val 415
Ser 385	Ala 370	Thr 385	Val 370	Ala 385	Arg 390	Met 405	Asn 410	Ser 410	Gln 410	Asp 410	Ser 410	Asn 415	Thr 415	Ser 415	Val 415	Val 415
Leu 420	Glu 435	Val 420	Val 435	Ser 420	Glu 435	Lys 440	Pro 440	Leu 440	Ser 440	Glu 440	Arg 440	Leu 445	Lys 445	Val 445	Val 445	Val 445
Pro 425	Gly 440	Glu 425	Thr 440	Ile 425	Asp 440	Pro 440	Ile 440	Pro 440	His 440	Gln 440	Leu 440	Leu 440	Arg 440	Lys 440	Tyr 440	Tyr 440
Ile 435	Gly 445	Tyr 435	Ala 445	Arg 435	Gln 445	Tyr 440	Val 440	Tyr 440	Pro 440	Arg 440	Leu 440	Ser 445	Thr 445	Glu 445	Ala 445	Ala 445
Ala 450	Arg 465	Val 450	Leu 465	Gln 450	Asp 465	Phe 470	Tyr 475	Leu 475	Glu 475	Leu 475	Arg 475	Lys 475	Gln 475	Ser 475	Gln 475	Gln 475
Arg 465	Leu 480	Asn 465	Ser 480	Ser 465	Pro 470	Ile 475	Thr 475	Thr 475	Arg 475	Gln 475	Leu 475	Glu 475	Ser 475	Leu 475	Ile 475	Ile 475
Arg 490	Leu 505	Thr 490	Glu 505	Ala 485	Arg 490	Ala 490	Arg 490	Leu 490	Glu 490	Leu 490	Arg 490	Glu 490	Glu 490	Ala 490	Thr 490	Thr 490
Lys 510	Glu 525	Asp 510	Ala 525	Glu 510	Asp 525	Ile 525	Val 525	Glu 525	Ile 525	Met 525	Lys 525	Tyr 525	Ser 525	Met 525	Leu 525	Leu 525
Gly 530	Thr 545	Tyr 530	Ser 545	Asp 530	Glu 545	Phe 545	Gly 545	Asn 545	Leu 545	Asp 545	Phe 545	Glu 545	Arg 545	Ser 545	Gln 545	Gln 545
His 550	Gly 565	Ser 550	Gly 565	Met 550	Ser 565	Asn 550	Arg 565	Ser 565	Thr 565	Ala 565	Lys 565	Arg 565	Phe 565	Ile 565	Ser 565	Ser 565
Ala 545	Leu 560	Asn 545	Asn 560	Val 545	Ala 550	Glu 550	Arg 550	Thr 550	Tyr 550	Asn 550	Asn 550	Ile 550	Phe 550	Gln 550	Phe 550	Phe 550
His 570	Gln 585	Leu 570	Arg 585	Gln 570	Ile 585	Ala 570	Lys 585	Glu 570	Leu 585	Asn 570	Ile 570	Gln 570	Val 570	Ala 570	Asp 570	Asp 570
Phe 590	Glu 605	Asn 590	Phe 605	Ile 590	Gly 590	Ser 590	Leu 590	Asn 590	Asp 590	Gln 590	Gly 590	Tyr 590	Leu 590	Leu 590	Lys 590	Lys 590
Lys 595	Gly 600	Pro 595	Lys 600	Val 595	Tyr 600	Gln 595	Leu 600	Gln 595	Thr 600	Met 600						

<210> 103

<211> 3408

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (725).. (1513)

<400> 103

120/175

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aagtgatagt	cttaatacta	gttttttagac	tagtcatttg	agaacagatg	attgatgtct	300
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121/175

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<210> 104

<211> 263

<212> PRT

<213> Homo sapiens

<400> 104

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Val Trp Ala Leu Leu Arg Arg Gln Ala Glu Leu Asp Gly Met Pro Ala
        35           40           45
Ile Asn Ala Lys Arg Val Tyr Arg Ile Met Arg Gln Asn Ala Leu Leu
       50           55           60
Leu Glu Arg Lys Pro Ala Val Pro Pro Ser Lys Arg Ala His Thr Gly
      65           70           75           80
Arg Val Ala Val Lys Glu Ser Asn Gln Arg Trp Cys Ser Asp Gly Phe
          85           90           95
Glu Phe Cys Cys Asp Asn Gly Glu Arg Leu Arg Val Thr Phe Ala Leu
        100          105          110
Asp Cys Cys Asp Arg Glu Ala Leu His Trp Ala Val Thr Thr Gly Gly
       115          120          125
Phe Asn Ser Glu Thr Val Gln Asp Val Met Leu Gly Ala Val Glu Arg
      130          135          140
Arg Phe Gly Asn Asp Leu Pro Ser Ser Pro Val Glu Trp Leu Thr Asp
     145          150          155          160
Asn Gly Ser Cys Tyr Arg Ala Asn Glu Thr Arg Gln Phe Ala Arg Met
          165          170          175
Leu Gly Leu Glu Pro Lys Asn Thr Ala Val Arg Ser Pro Glu Ser Asn
        180          185          190
Gly Ile Ala Glu Ser Phe Val Lys Thr Ile Lys Arg Asp Tyr Ile Ser
       195          200          205
Ile Met Pro Lys Pro Asp Gly Leu Thr Ala Ala Lys Asn Leu Ala Glu
      210          215          220
Ala Phe Glu His Tyr Asn Glu Trp His Pro His Ser Ala Leu Gly Tyr
     225          230          235          240
Arg Ser Pro Arg Glu Tyr Leu Arg Gln Arg Ala Cys Asn Gly Leu Ser

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122/175

245
Asp Asn Arg Cys Leu Glu Ile
260

250

255

<210> 105
<211> 3338
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (201).. (1904)

<400> 105

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gggcccgggtg cggctgtgtg gggtcggggag cggagttgca gaatccaagg acccattttg 180
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atgtgacatt gagagtagag cagaaagact tccctgcccc tccgattgtg ctggctgcoct 360
gtagtgatta cttctgtgcc atgttcacta gtgagctctc agagaagggg aaaccttatg 420
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aaacggtaca tgtgacagtg gagaatgtac aagaactgct tcctgcagcc tgtctgcttc 540
agttgaaagg tgtgaaacaa gcctgctgtg agttcttaga aagtcagttg gacctttcta 600
attgcctggg tattagggat tttgctgaaa ccacaaattg tgttgacctg atgcaagcag 660
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accatccaga gctagtgacc agtccagtgg acagtttagt ggagtatcaa aaatcctttc 1980
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123/175

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<210> 106

<211> 568

<212> PRT

<213> Homo sapiens

<400> 106

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Met Gly Gly Ile Met Ala Pro Lys Asp Ile Met Thr Asn Thr His Ala
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Lys Ser Ile Leu Asn Ser Met Asn Ser Leu Arg Lys Ser Asn Thr Leu
          20           25           30
Cys Asp Val Thr Leu Arg Val Glu Gln Lys Asp Phe Pro Ala His Arg
          35           40           45
Ile Val Leu Ala Ala Cys Ser Asp Tyr Phe Cys Ala Met Phe Thr Ser
          50           55           60
Glu Leu Ser Glu Lys Gly Lys Pro Tyr Val Asp Ile Gln Gly Leu Thr
          65           70           75           80
Ala Ser Thr Met Glu Ile Leu Leu Asp Phe Val Tyr Thr Glu Thr Val
          85           90           95
His Val Thr Val Glu Asn Val Gln Glu Leu Leu Pro Ala Ala Cys Leu
          100          105          110
Leu Gln Leu Lys Gly Val Lys Gln Ala Cys Cys Glu Phe Leu Glu Ser
          115          120          125
Gln L u Asp Pro Ser Asn Cys Leu Gly Ile Arg Asp Phe Ala Glu Thr

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124/175

130		135		140
His Asn Cys Val Asp	Leu Met Gln Ala Ala Glu	Val Phe Ser Gln Lys		
145	150	155	160	
His Phe Pro Glu Val	Val Gln His Glu Glu Phe	Ile Leu Leu Ser Gln		
	165	170	175	
Gly Glu Val Glu Lys	Leu Ile Lys Cys Asp Glu	Ile Gln Val Asp Ser		
	180	185	190	
Glu Glu Pro Val Phe	Glu Ala Val Ile Asn Trp	Val Lys His Ala Lys		
	195	200	205	
Lys Glu Arg Glu Glu	Ser Leu Pro Asn Leu Leu	Gln Tyr Val Arg Met		
	210	215	220	
Pro Leu Leu Thr Pro	Arg Tyr Ile Thr Asp	Val Ile Asp Ala Glu Pro		
225	230	235	240	
Phe Ile Arg Cys Ser	Leu Gln Cys Arg Asp	Leu Val Asp Glu Ala Lys		
	245	250	255	
Lys Phe His Leu Arg	Pro Glu Leu Arg Ser	Gln Met Gln Gly Pro Arg		
	260	265	270	
Thr Arg Ala Arg Leu	Gly Ala Asn Glu Val	Leu Leu Val Val Gly Gly		
	275	280	285	
Phe Gly Ser Gln Gln	Ser Pro Ile Asp Val	Val Glu Lys Tyr Asp Pro		
	290	295	300	
Lys Thr Gln Glu Trp	Ser Phe Leu Pro Ser	Ile Thr Arg Lys Arg Arg		
305	310	315	320	
Tyr Val Ala Ser Val	Ser Leu His Asp Arg	Ile Tyr Val Ile Gly Gly		
	325	330	335	
Tyr Asp Gly Arg Ser	Arg Leu Ser Ser	Val Glu Cys Leu Asp Tyr Thr		
	340	345	350	
Ala Asp Glu Asp Gly	Val Trp Tyr Ser	Val Ala Pro Met Asn Val Arg		
	355	360	365	
Arg Gly Leu Ala Gly	Ala Thr Thr Leu Gly	Asp Met Ile Tyr Val Ser		
	370	375	380	
Gly Gly Phe Asp Gly	Ser Arg Arg His Thr	Ser Met Glu Arg Tyr Asp		
385	390	395	400	
Pro Asn Ile Asp Gln	Trp Ser Met Leu Gly	Asp Met Gln Thr Ala Arg		
	405	410	415	
Glu Gly Ala Gly Leu	Val Val Ala Ser	Gly Val Ile Tyr Cys Leu Gly		
	420	425	430	
Gly Tyr Asp Gly Leu	Asn Ile Leu Asn	Ser Val Glu Lys Tyr Asp Pro		
	435	440	445	
His Thr Gly His Trp	Thr Asn Val Thr Pro	Met Ala Thr Lys Arg Ser		
	450	455	460	
Gly Ala Gly Val Ala	Leu Leu Asn Asp His	Ile Tyr Val Val Gly Gly		
465	470	475	480	
Phe Asp Gly Thr Ala	His Leu Ser Ser	Val Glu Ala Tyr Asn Ile Arg		
	485	490	495	
Thr Asp Ser Trp Thr	Thr Val Thr Ser	Met Thr Thr Pro Arg Cys Tyr		
	500	505	510	
Val Gly Ala Thr Val	Leu Arg Gly Arg	Leu Tyr Ala Ile Ala Gly Tyr		

125/175

	515		520		525
Asp	Gly Asn Ser Leu Leu Ser Ser Ile Glu Cys Tyr Asp Pro Ile Ile				
530		535		540	
Asp Ser Trp Glu Val Val Thr Ser Met Gly Thr Gln Arg Cys Asp Ala					
545		550		555	560
Gly Val Cys Val Leu Arg Glu Lys					
	565				

<210> 107

<211> 2925

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72).. (1160)

<400> 107

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tatctgacct catggatgaa cttcaggatg ttcagctcac agagatcaaa ccacttctaa 120
atgataagga acatgatata gaaacaactc atggtgtggt ccacgtcact ataagaggct 180
tacccaaagg aaacagacca gttatactaa catatcatga cattggcctc aaccataaat 240
cctgttccaa tgcattcttt aactttgagg atatgcaaga gatcaccag cactttgctg 300
tctgtcatgt ggatgcccc aagcagcagg aaggtgcacc ctctttccca acagggtatc 360
agtacccac aatggatgag ctggctgaaa tgctgcctcc tgttcttacc cacctaagcc 420
tgaaaagcat cattggaatt ggagttggag ctggagctta catcctcagc agatttgac 480
tcaaccatcc agagcttgtg gaaggccttg tgctcattaa tgttgaccct tgcgctaaag 540
gctggattga ctgggcagct tccaaactct ctggcctgac aaccaatgtt gtggacatta 600
ttttggctca tcactttggg caggaagagt tacaggccaa cctggacctg atccaaacct 660
acagaatgca tattgcccc aacatcaacc aagacaacct gcagctcttc ttgaattcct 720
acaatggacg cagagacctg gagatcgaaa gaccatact gggccaaaat gataacaaat 780
caaaaacatt aaagtgttct actttacttg tggtagggga caattcgcct gcagttgagg 840
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tgcaaagtga ttccaggaga gacgagcttt gaggaatgtg gaaaatcata attgccgtct 1740

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126/175

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tgtggtttta ttactggact ctcttagcac aggaaggtgg aaacaaaatg ccaggcctct 1980
gctctgaaga gcaaaactgc tgcgctgca gtatctgata ccagacatcc acatatccac 2040
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<210> 108

<211> 363

<212> PRT

<213> Homo sapiens

<400> 108

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Met Asp Glu Leu Gln Asp Val Gln Leu Thr Glu Ile Lys Pro Leu Leu
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Asn Asp Lys Glu His Asp Ile Glu Thr Thr His Gly Val Val His Val
      20             25             30
Thr Ile Arg Gly Leu Pro Lys Gly Asn Arg Pro Val Ile Leu Thr Tyr
      35             40             45
His Asp Ile Gly Leu Asn His Lys Ser Cys Ser Asn Ala Phe Phe Asn
      50             55             60
Phe Glu Asp Met Gln Glu Ile Thr Gln His Phe Ala Val Cys His Val
      65             70             75             80
Asp Ala Pro Gly Gln Gln Glu Gly Ala Pro Ser Phe Pro Thr Gly Tyr
      85             90             95
Gln Tyr Pro Thr Met Asp Glu Leu Ala Glu Met Leu Pro Pro Val Leu
      100            105            110
Thr His Leu Ser Leu Lys Ser Ile Ile Gly Ile Gly Val Gly Ala Gly
      115            120            125
Ala Tyr Ile Leu Ser Arg Phe Ala Leu Asn His Pro Glu Leu Val Glu
      130            135            140
Gly Leu Val Leu Ile Asn Val Asp Pro Cys Ala Lys Gly Trp Ile Asp
      145            150            155            160

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127/175

Trp Ala Ala Ser Lys Leu Ser Gly Leu Thr Thr Asn Val Val Asp Ile
 165 170 175
 Ile Leu Ala His His Phe Gly Gln Glu Glu Leu Gln Ala Asn Leu Asp
 180 185 190
 Leu Ile Gln Thr Tyr Arg Met His Ile Ala Gln Asp Ile Asn Gln Asp
 195 200 205
 Asn Leu Gln Leu Phe Leu Asn Ser Tyr Asn Gly Arg Arg Asp Leu Glu
 210 215 220
 Ile Glu Arg Pro Ile Leu Gly Gln Asn Asp Asn Lys Ser Lys Thr Leu
 225 230 235 240
 Lys Cys Ser Thr Leu Leu Val Val Gly Asp Asn Ser Pro Ala Val Glu
 245 250 255
 Ala Val Val Glu Cys Asn Ser Arg Leu Asn Pro Ile Asn Thr Thr Leu
 260 265 270
 Leu Lys Met Ala Asp Cys Gly Gly Leu Pro Gln Val Val Gln Pro Gly
 275 280 285
 Lys Leu Thr Glu Ala Phe Lys Tyr Phe Leu Gln Gly Met Gly Tyr Ile
 290 295 300
 Pro Ser Ala Ser Met Thr Arg Leu Ala Arg Ser Arg Thr His Ser Thr
 305 310 315 320
 Ser Ser Ser Leu Gly Ser Gly Glu Ser Pro Phe Ser Arg Ser Val Thr
 325 330 335
 Ser Asn Gln Ser Asp Gly Thr Gln Glu Ser Cys Glu Ser Pro Asp Val
 340 345 350
 Leu Asp Arg His Gln Thr Met Glu Val Ser Cys
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<210> 109

<211> 2677

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (240).. (1001)

<400> 109

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 gaaaaattga tgtacttcaa gctgaagtag ctgcattgaa gacacttgta ttgtccagtt 360
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 tacagccaat tgtaaaagac tgcaaagagg ctgacttata cttgtataat gaattccgat 540
 tgtggaagga tgagcccaca atggacagga cgtgtccttt cttagacaaa atctaccagg 600

128/175

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```

<210> 110

<211> 254

<212> PRT

<213> Homo sapiens

<400> 110

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Met Val Arg Glu Ala Asn Ile Lys Gln Ala Thr Ala Glu Lys Gln Leu
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Lys Glu Ala Gln Gly Lys Ile Asp Val Leu Gln Ala Glu Val Ala Ala
          20             25             30
Leu Lys Thr Leu Val Leu Ser Ser Ser Pro Thr Ser Pro Thr Gln Glu

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129/175

```

          35          40          45
Pro Leu Pro Gly Gly Lys Thr Pro Phe Lys Lys Gly His Thr Arg Asn
   50          55          60
Lys Ser Thr Ser Ser Ala Met Ser Gly Ser His Gln Asp Leu Ser Val
   65          70          75          80
Ile Gln Pro Ile Val Lys Asp Cys Lys Glu Ala Asp Leu Ser Leu Tyr
          85          90          95
Asn Glu Phe Arg Leu Trp Lys Asp Glu Pro Thr Met Asp Arg Thr Cys
          100          105          110
Pro Phe Leu Asp Lys Ile Tyr Gln Glu Asp Ile Phe Pro Cys Leu Thr
          115          120          125
Phe Ser Lys Ser Glu Leu Ala Ser Ala Val Leu Glu Ala Val Glu Asn
          130          135          140
Asn Thr Leu Ser Ile Glu Pro Val Gly Leu Gln Pro Ile Arg Phe Val
          145          150          155          160
Lys Ala Ser Ala Val Glu Cys Gly Gly Pro Lys Lys Cys Ala Leu Thr
          165          170          175
Gly Gln Ser Lys Ser Cys Lys His Arg Ile Lys Leu Gly Asp Ser Ser
          180          185          190
Asn Tyr Tyr Tyr Ile Ser Pro Phe Cys Arg Tyr Arg Ile Thr Ser Val
          195          200          205
Cys Asn Phe Phe Thr Tyr Ile Arg Tyr Ile Gln Gln Gly Leu Val Lys
          210          215          220
Gln Gln Asp Val Asp Gln Met Phe Trp Glu Val Met Gln Leu Arg Lys
          225          230          235          240
Glu Met Ser Leu Ala Lys Leu Gly Tyr Phe Lys Glu Glu Leu
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<210> 111

<211> 3448

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (104).. (1057)

<400> 111

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130/175

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131/175

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3448

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<211> 318

<212> PRT

<213> Homo sapiens

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132/175

305

310

315

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 <212> DNA
 <213> Homo sapiens

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133/175

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<210> 114

<211> 793

<212> PRT

<213> Homo sapiens

<400> 114

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Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly Asp Phe Leu Lys Ile
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Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu Asp Leu Arg Lys Lys Tyr
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Asp Lys Tyr Gly Glu Lys Gly Leu Glu Asp Asn Gln Gly Gly Gln Tyr
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Pro Glu Ile Ile Thr Leu Glu Arg Arg Glu Phe Asp Ala Ala Val Asn
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134/175

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Leu	Ser	Ala	Asn	Thr	Leu	Glu	Asp	Arg	Leu	Ala	His	His	Arg	Trp	Leu
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Leu	Phe	Phe	His	Phe	Gly	Lys	Asn	Glu	Asn	Ser	Asn	Asp	Pro	Glu	Leu
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135/175

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 565 570 575
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 Gln Glu Asn Val Gln Arg Tyr Pro Glu Ile Arg Phe Phe Pro Pro Lys
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 Thr Asp Leu Thr Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys
 675 680 685
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<212> DNA

<213> Homo sapiens

<220>

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136/175

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<210> 116

<211> 380

<212> PRT

<213> Homo sapiens

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          20           25           30
Ala Lys Leu Cys Glu Pro Gln Trp Phe Tyr Glu Glu Thr Glu Ser Ser
          35           40           45
Asp Asp Val Glu Val Leu Thr Leu Lys Lys Phe Lys Gly Asp Leu Ala
          50           55           60
Tyr Arg Arg Gln Glu Tyr Gln Lys Ala Leu Gln Glu Tyr Ser Ser Ile
          65           70           75           80
Ser Glu Lys Leu Ser Ser Thr Asn Phe Ala Met Lys Arg Asp Val Gln
          85           90           95
Glu Gly Gln Ala Arg Cys Leu Ala His Leu Gly Arg His Met Glu Ala
          100          105          110
Leu Glu Ile Ala Ala Asn Leu Glu Asn Lys Ala Thr Asn Thr Asp His
          115          120          125
Leu Thr Thr Val Leu Tyr Leu Gln Leu Ala Ile Cys Ser Ser Leu Gln
          130          135          140
Asn Leu Glu Lys Thr Ile Phe Cys Leu Gln Lys Leu Ile Ser Leu His
          145          150          155          160

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137/175

Pro Phe Asn Pro Trp Asn Trp Gly Lys Leu Ala Glu Ala Tyr Leu Asn
 165 170 175
 Leu Gly Pro Ala Leu Ser Ala Ala Leu Ala Ser Ser Gln Lys Gln His
 180 185 190
 Ser Phe Thr Ser Ser Asp Lys Thr Ile Lys Ser Phe Phe Pro His Ser
 195 200 205
 Gly Lys Asp Cys Leu Leu Cys Phe Pro Glu Thr Leu Pro Glu Ser Ser
 210 215 220
 Leu Phe Ser Val Glu Ala Asn Ser Ser Asn Ser Gln Lys Asn Glu Lys
 225 230 235 240
 Ala Leu Thr Asn Ile Gln Asn Cys Met Ala Glu Lys Arg Glu Thr Val
 245 250 255
 Leu Ile Glu Thr Gln Leu Lys Ala Cys Ala Ser Phe Ile Arg Thr Arg
 260 265 270
 Leu Leu Leu Gln Phe Thr Gln Pro Gln Gln Thr Ser Phe Ala Leu Glu
 275 280 285
 Arg Asn Leu Arg Thr Gln Gln Glu Ile Glu Asp Lys Met Lys Gly Phe
 290 295 300
 Ser Phe Lys Glu Asp Thr Leu Leu Leu Ile Ala Glu Val Met Gly Glu
 305 310 315 320
 Asp Ile Pro Glu Lys Ile Lys Asp Glu Val His Pro Glu Val Lys Cys
 325 330 335
 Val Gly Ser Val Ala Leu Thr Ala Leu Val Thr Val Ser Ser Glu Glu
 340 345 350
 Phe Glu Asp Lys Trp Phe Arg Lys Ile Lys Asp His Phe Cys Pro Phe
 355 360 365
 Glu Asn Gln Phe His Thr Glu Ile Gln Ile Leu Ala
 370 375 380

<210> 117

<211> 1836

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (283).. (732)

<400> 117

cacttaacac actcttgatg acatatggca ggttcttggt attgacaccc gtgtggctgc 60
 aggtggcatg aatcatgcat ggcttgctct gatctgtctt ctgcagagcc cattctctct 120
 gtcttttgct agtctggact ggagagcaac ttccctgagt caggactctt gctgctaatt 180
 gcagaaaacc agcagtcctt gtgaagtgt ggtgttctca gatttcagct gtaaaatata 240
 gaatcctcat taattgtatt tacaactata ttgagcaaac caatgttggt ctttattaat 300
 gtacagacca aaaaagacac ctcaaaagaa aggacgtacg cgtttcttgt aaacacgagg 360
 caccccaaga taagaagaca gatagagcaa gggatggaca tggtcacctc ctcagtgtat 420
 ggagaaaagt accggcttca gtttgatttt caagaggcag tgaagaattt cttcccccca 480



138/175

```

ggaaatgaag tggттаатгг agaaaattta agctttgcat atgaattcaa agctgatgca 540
ttatttgatt tcttctattg gtttgggctc agtaattccg ttgtaaaagt aaatggaaaa 600
gttcttttag gttcaataga tgatgttttt aactgcaatc tgtcacccag atcatctctg 660
acagagcctc ttttggcaga attaccattt ccaagtgttc tggaatctga agagacaccc 720
aaccaattta tctgattgaa ctgaacattg tagcagttgc tcccgcactc caggcctgtg 780
ctagactata ggctgggggg agggtaggag gtgggaggca gatacttcca cctgcgtgtc 840
aatctccggc tcttccatgg cttctatgga ggactcctct cttctgcttc tgtggatgtg 900
atgccctggc aggcccaggg cagctgattc ccctaaaact tatgattacc aggatggaaa 960
ggccttggto ccatggcaact ggggtggggct gggggatatt ctctactttg aacacttctc 1020
ccaagaggca gaagggccac agagtctctc caccctgaac atttttctca gttccctggg 1080
agtttttgtg gcagcctttg tgggagtggc ctgactggct gttgacctag catgcttcat 1140
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aaggggttaa gagttctgtt ctcttgccaa cctggctggg caaaagcctg tgccatcttt 1260
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cccttggcct cctctttaac taagtgacct atgtagaagg aagccaggag atatggtacc 1440
gaacaatgac aggggaaggg tattggacac ggcagcgtcc tccttattga aaacacatta 1500
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ataatgagga agagttagtg gtcctgagtg taatttttta tcctttctta aaaagtttct 1740
gtattatgoa ttttgataac actactgatg atccttccac ttacatttga aatgttatgt 1800
accacatttg cacaattaaa acttttctta gcattc 1836

```

<210> 118

<211> 150

<212> PRT

<213> Homo sapiens

<400> 118

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Met Leu Phe Phe Ile Asn Val Gln Thr Lys Lys Asp Thr Ser Lys Glu
  1             5             10             15
Arg Thr Tyr Ala Phe Leu Val Asn Thr Arg His Pro Lys Ile Arg Arg
          20             25             30
Gln Ile Glu Gln Gly Met Asp Met Val Ile Ser Ser Val Ile Gly Glu
      35             40             45
Ser Tyr Arg Leu Gln Phe Asp Phe Gln Glu Ala Val Lys Asn Phe Phe
    50             55             60
Pro Pro Gly Asn Glu Val Val Asn Gly Glu Asn Leu Ser Phe Ala Tyr
    65             70             75             80
Glu Phe Lys Ala Asp Ala Leu Phe Asp Phe Phe Tyr Trp Phe Gly Leu
          85             90             95
Ser Asn Ser Val Val Lys Val Asn Gly Lys Val Leu Leu Gly Ser Ile
    100             105             110
Asp Asp Val Phe Asn Cys Asn Leu Ser Pro Arg Ser Ser Leu Thr Glu
    115             120             125
Pro Leu Leu Ala Glu L u Pro Phe Pro Ser Val Leu Glu Ser Glu Glu

```



139/175

130
Thr Pro Asn Gln Phe Ile
145

135

150

140

<210> 119
<211> 1863
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (460).. (1233)

<400> 119
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agcgcgttgg gccccgcggg cgatgcccg cgccgcctcc tcggagcggc ggccaagtgt 180
gaacttggcg tcggcctgga gccccgagca gcccgggggc ggccggcccg aggcgagcgg 240
cgatgagatg tgtgcacaga cccaggccat gcagatactg gtgcctctaa cttcgtcagc 300
ccttagaaca tgacttgctg tccccagtgg agaagaaacc agaagctaca gccaaagtatg 360
tcccctccaa agtccatttc tgttcagtgc ctgaaaatga ggaggatgcc tccctgaaga 420
gacatctcac acctcccaa ggcaacagcc cacattccaa tgagagaaaag agcaccccca 480
cctcctccac cgagtcagga aaccccggtg tatagcatgg atgacttccc tccacctcct 540
ccccacactg tatgtgaggg gcagctggac agtgaggatc ccgagggggc acgccccagc 600
ttcaacaaac tttctaaagt gacaattgca agggaaaggc acatgcctgg tgcagcccat 660
gtggtaggta gtcagacact ggcttcaga ctccaaactt ctatcaaggg ttcagaggct 720
gagtccacac caccctcctt catgagcgtt cagccccaac ttgctgggtc tcttgggtggg 780
cagccagcac ccatccagac tcaaagcctc agccatgatc cagtcagtgg aactcagggt 840
ttagaaaaga aagtcagtcc tgatcctcag aagagttcag aagacatcag aacagaggct 900
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aggctgaaga caacaatgga cctgatggaa ggttttattc cccgagatgt gaacttgctg 1020
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ggcaagagga atgaagacaa ggaagcagtg agcatgttgg ttaactgccc tcagatttca 1140
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ggggctgtac tttcagtggg attttcccaa cattaacctc tccactttta cctcttctaa 1260
aatacccaac caaaagatca ctgtttctct caacactatt taatctgaaa aatgtttcag 1320
tacaaccac tgtttgaact atctgggtta ttgggtgttg ttctgatga aaggaaaaaa 1380
aattctctcc aggaggaagc ctttttctt cttgcccttc ctgattgatc ttctgagagc 1440
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tgaaactgag aactgattgg aggggtgttg atcatttagt ttttaacagg ctgaggcaac 1560
atggatcagt gtgtgtcccc ctccaggaatg tatccacagt ggccttccct gctggtgggc 1620
agtgtatcct gatggcaggg tacaagtacc attaatgaag ggtctgcaac ataaagcctt 1680
aaaaagacac acactaagaa aactgtaaaa cttgaaacat tgttatttat attttttaaa 1740
atggaaaaga tcaactatgt tttgtgtcta accacttatt tgattctgtt ttgtggtgga 1800
catagatgat tacgtttgag ctttgtattt tgtgaaaacc ttaatgaaat gaattccaaa 1860
gat 1863



140/175

<210> 120
 <211> 258
 <212> PRT
 <213> Homo sapiens

<400> 120
 Met Arg Glu Arg Ala Pro Pro Pro Pro Pro Pro Ser Gln Glu Thr Pro
 1 5 10 15
 Val Tyr Ser Met Asp Asp Phe Pro Pro Pro Pro His Thr Val Cys
 20 25 30
 Glu Ala Gln Leu Asp Ser Glu Asp Pro Glu Gly Pro Arg Pro Ser Phe
 35 40 45
 Asn Lys Leu Ser Lys Val Thr Ile Ala Arg Glu Arg His Met Pro Gly
 50 55 60
 Ala Ala His Val Val Gly Ser Gln Thr Leu Ala Ser Arg Leu Gln Thr
 65 70 75 80
 Ser Ile Lys Gly Ser Glu Ala Glu Ser Thr Pro Pro Ser Phe Met Ser
 85 90 95
 Val His Ala Gln Leu Ala Gly Ser Leu Gly Gly Gln Pro Ala Pro Ile
 100 105 110
 Gln Thr Gln Ser Leu Ser His Asp Pro Val Ser Gly Thr Gln Gly Leu
 115 120 125
 Glu Lys Lys Val Ser Pro Asp Pro Gln Lys Ser Ser Glu Asp Ile Arg
 130 135 140
 Thr Glu Ala Leu Ala Lys Glu Ile Val His Gln Asp Lys Ser Leu Ala
 145 150 155 160
 Asp Ile Leu Asp Pro Asp Ser Arg Leu Lys Thr Thr Met Asp Leu Met
 165 170 175
 Glu Gly Leu Phe Pro Arg Asp Val Asn Leu Leu Lys Glu Asn Ser Val
 180 185 190
 Lys Arg Lys Ala Ile Gln Arg Thr Val Ser Ser Ser Gly Cys Glu Gly
 195 200 205
 Lys Arg Asn Glu Asp Lys Glu Ala Val Ser Met Leu Val Asn Cys Pro
 210 215 220
 Gln Ile Ser Phe Pro Arg Leu Gly Pro Trp Leu Cys Pro Gln Thr Ser
 225 230 235 240
 Arg Val Ser Pro Phe Leu Leu Gly Ala Val Leu Ser Val Val Phe Ser
 245 250 255
 Gln His

<210> 121
 <211> 2203
 <212> DNA
 <213> Homo sapiens



141/175

<220>

<221> CDS

<222> (91).. (564)

<400> 121

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gctcaggctc ggataggggg caagggtaca gctcgcagaa agaagaagg ggtacataga 180
acagccacag ctgatgacaa aaagcttcag agttctctaa aaaaactggc tgtgaataat 240
atagctggta ttgaagaggt gaacatgatt aaagatgatg ggacagttat tcatttcaac 300
aatcccaaag tccaagcttc ctttctgct aataccttg caattactgg tcatgcagaa 360
gccaaaccaa tcacagaaat gcttcctgga atattaagtc agcttgggtgc tgacagtta 420
acaagcctta ggaagttagc tgaacagttc ccacggcaag tcttggacag taaagcacca 480
aaaccagagg acattgatga ggaagatgat gatgttcag atctttaga aaattttgat 540
gaggcatcaa agaatgaagc taactaaaag tttggttttt ggaagctggc atggactaga 600
tttaacaaat cagctatgtg gttccaaagt ttacagaca tggagaacat cacctgttac 660
tagttcagta atataaatat tttgtatatt aataatgctg tttgttcagc atttttcgg 720
catttgattt tgcattttgc acttcctccc aggatatttt tttgggtcaaa atatgaagta 780
ttgggtcagt ttgagggtgt tttggttttt gattcctggg ttttttgtt tttgtttggg 840
gtatttttgg tgtatgtatg tttatgtatg tgtgtgggta tgtgtgtata cagtgagag 900
caaattggaa aacagttcta tttatcctcc tccctcccca gtagaaataa aaaaaatctt 960
tacatttgtt acttttcttt tcccccgta agacacagaa ttaatggaaa gtgagtatct 1020
tggatttcaa atctgaagag atttttacca ttagtgggtt gattttaatt tgcttggta 1080
actatcatat tttcatata cttctctgga tttaaaatat cttgaggtat tttgccactg 1140
gcttcagct ggagtaatgg gtaacatatc tttggtatgg ttgcottaga ttaacttacc 1200
tagtcagacc cagaagaact tcttttacta gcttgcttcc taaatgcctt ttttctctc 1260
cttttggctc ccaaattggc tggtcagctt ttggtaatat tcttctcat cttccacct 1320
gcttgagaag gatgttctcc atatagagtt tagcgagtgc ctaatccctc cttttgtaag 1380
attttgttcc ctgagcttga ggaacaact catcttcaac tttttatttc tccctgatgt 1440
tacagtttgg tagatttcaa actggaatag ctgcatgtg cttgctaaat aattttatgc 1500
cagccttctc ctgtatccta gctgttctta acagcaggta caaaaatgcc tgtttttcag 1560
caagggtgaa attgggaatg tccttttgaa tcagaagaaa ataggccata gactcatctc 1620
ccagcacaaa tgggcattct atgaaatggg actggcccta ggaggatttc ctcaaccact 1680
ctcctactct tggccttgaa cctacctctg ggttggatct tactattgta gctgctcact 1740
ataccctcct gcatgcttag aataatgctt tgaggggagc actggtaaaa cacagtattt 1800
atttttttac ctcttttaag aggacttgga ggtaagttgc attcattcac tcaagtttcc 1860
ctcttgctgt ctaatagaag cttacttttt gctatatcag ctttgttac agccaatatt 1920
taaggacaaa atttagaaaa tatatcattt cctggcccat catcaaacta atacagctta 1980
acctgcagc taccaatttt tgtgtcaagc tagatatctt tatttgatat ctaaggtgca 2040
agaccaacaa tatattaaga gatctgtaga catgaaggca aagctcttgt attttttttc 2100
atccaaacac ctcaatttat tttataaatt cgttcatttt tcctgttatg ttttatataa 2160
tatatggact aaacaaaata aaataacagt gcaaaagaga aac 2203
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<210> 122

<211> 158

<212> PRT

<213> Homo sapiens



142/175

<400> 122

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Met Asn Gln Glu Lys Leu Ala Lys Leu Gln Ala Gln Val Arg Ile Gly
 1           5           10           15
Gly Lys Gly Thr Ala Arg Arg Lys Lys Val Val His Arg Thr Ala
 20           25           30
Thr Ala Asp Asp Lys Lys Leu Gln Ser Ser Leu Lys Lys Leu Ala Val
 35           40           45
Asn Asn Ile Ala Gly Ile Glu Glu Val Asn Met Ile Lys Asp Asp Gly
 50           55           60
Thr Val Ile His Phe Asn Asn Pro Lys Val Gln Ala Ser Leu Ser Ala
 65           70           75           80
Asn Thr Phe Ala Ile Thr Gly His Ala Glu Ala Lys Pro Ile Thr Glu
 85           90           95
Met Leu Pro Gly Ile Leu Ser Gln Leu Gly Ala Asp Ser Leu Thr Ser
100          105          110
Leu Arg Lys Leu Ala Glu Gln Phe Pro Arg Gln Val Leu Asp Ser Lys
115          120          125
Ala Pro Lys Pro Glu Asp Ile Asp Glu Glu Asp Asp Asp Val Pro Asp
130          135          140
Leu Val Glu Asn Phe Asp Glu Ala Ser Lys Asn Glu Ala Asn
145          150          155

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<210> 123

<211> 1696

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (62).. (898)

<400> 123

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ctgcttcggg gcctcggggc agccgctggc gctgccaggc cgagtgtctg tgggcgaggg 180
cgtgctgacc aaagagtgcc gcaagaaggc caagccgcgc atcctcttcc tctttaacga 240
catcctggtg tatggcagca tcgtgctcaa caagcgcaag taccgcagcc agcacatcat 300
ccccctggag gaggtcacac tggagctgtt gccggagacg ctgcaggcca agaaccgctg 360
gatgatcaag acggccaaga agtcctttgt ggtgtcggcc gcctccgcta cggagcgcca 420
ggaatggatt agccacatcg aggagtgcgt gcggcggcaa ctgaggggcca cgggcccgcc 480
gccagcacg gagcacgcgg caccctggat ccccgacaag gccacggaca tctgcatgcg 540
ctgcacgcag acgcgcttct ctgccctcac gaggcgccac cactgccgca agtggcgctt 600
cgtggtctgc gctgagtgtc cgcgccagcg cticctgtct ccgcgcctgt cccccaagcc 660
cgtgcgcgtc tgcagcctct gctaccgcga actggccgcc cagcagcggc aggaggaggc 720
ggaggagcag ggcgcggggt cccagggcga gccagcccac ctggcccggc ccatctgcgg 780
agcgtccagt ggagatgacg atgactccga cgaggacaag gagggcagca gggacggcga 840

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)
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143/175

```

ctggcccagc agcgtggagt tctacgcctc gggggtggcc tggctctgcct tccacagctg 900
acccccggcc tgcagaacat ctgtcccca gccagctcca ctgcccaggc ccctaagagg 960
gcagctccag aagctgcca gggctccggg accccatccc atggtggcag gtgcagcggg 1020
ggggagtggc tctttctgga ctcccagtgc ctttttgctg gacactgtgt ccttatggct 1080
tactgcagg taatgccttt cccttcagga agcccagaa caccacagg tcttggtaac 1140
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cgaccccagg tctccagaca tctagggacc agagcaggtt tgggaacaca gagggaagac 1260
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gcctttttgt cctgtcctca gctctccgtg tggtcagcga aaccattgtt ttctgttagg 1620
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tgggtggttg caaac                                     1696

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<210> 124

<211> 279

<212> PRT

<213> Homo sapiens

<400> 124

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Met Val Asp His Leu Ala Asn Thr Glu Ile Asn Ser Gln Arg Ile Ala
 1           5           10           15
Ala Val Glu Ser Cys Phe Gly Ala Ser Gly Gln Pro Leu Ala Leu Pro
          20           25           30
Gly Arg Val Leu Leu Gly Glu Gly Val Leu Thr Lys Glu Cys Arg Lys
          35           40           45
Lys Ala Lys Pro Arg Ile Leu Phe Leu Phe Asn Asp Ile Leu Val Tyr
          50           55           60
Gly Ser Ile Val Leu Asn Lys Arg Lys Tyr Arg Ser Gln His Ile Ile
          65           70           75           80
Pro Leu Glu Glu Val Thr Leu Glu Leu Leu Pro Glu Thr Leu Gln Ala
          85           90           95
Lys Asn Arg Trp Met Ile Lys Thr Ala Lys Lys Ser Phe Val Val Ser
          100          105          110
Ala Ala Ser Ala Thr Glu Arg Gln Glu Trp Ile Ser His Ile Glu Glu
          115          120          125
Cys Val Arg Arg Gln Leu Arg Ala Thr Gly Arg Pro Pro Ser Thr Glu
          130          135          140
His Ala Ala Pro Trp Ile Pro Asp Lys Ala Thr Asp Ile Cys Met Arg
          145          150          155          160
Cys Thr Gln Thr Arg Phe Ser Ala Leu Thr Arg Arg His His Cys Arg
          165          170          175
Lys Cys Gly Phe Val Val Cys Ala Glu Cys Ser Arg Gln Arg Phe Leu
          180          185          190
Leu Pro Arg Leu Ser Pro Lys Pro Val Arg Val Cys Ser Leu Cys Tyr

```


144/175

	195		200		205	
Arg	Glu	Leu	Ala	Ala	Gln	Gln
	210				215	
Ala	Gly	Ser	Pro	Gly	Gln	Pro
225				230		
Ala	Ser	Ser	Gly	Asp	Asp	Asp
			245		250	
Arg	Asp	Gly	Asp	Trp	Pro	Ser
	260			265		
Ala	Trp	Ser	Ala	Phe	His	Ser
	275					

<210> 125

<211> 3078

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1668).. (2561)

<400> 125

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tgctottttg agcagctttg catgacacgc tctggtaaaa ggtgtgcac tttaaattat 180
ttcatggata ctttgaaaaa tattgtatca cttcaaatag agcaataagt ttatatgttc 240
tcaagatttc atttgttttt aagaatttta agttcgtgga ttaatatcac tacttgaata 300
ctgacagtgg ttgattagac accgaaaggt tactgattgt tgaatgtatc tgtgttagag 360
ctgtgcactg gcacgcttgc atcagggggt ggggccacac ggccgccaca cagattcccc 420
cgtgatgcct ggagctgctt ccagagccgg gtgtctccaa gaggcacctg taggacttcc 480
catttagaaa tctcttgagt gggtttgtat gttaccttct ccaaggitta ttaggacag 540
agatattgct ggaaggctcat gggtcagatt ccctcacaac ccacctctgc tgcgggtgca 600
gccccactcc aaggctcccc gttattgggg tatgtgagga gcagtaaata taaaaccagt 660
tcaactgtcc tcatggaatc accctttctg tttttgcagt attcataaag ctagtgttaag 720
gtctggtttt agtctattaa atcttagaga tctaaaggaa atgtcaaaa tgtagccagg 780
ttttaaatgc ttttaacttt aaaaaatgta aatttttgta tgtttatagc ttctaaatat 840
gaaagttaaa gaatgtactg tgatgaaatg ttcagtatta tgttgcttct cagtatcatg 900
ttgcttctca gtattgtgtt gottctgatt ctatgaatgt tcattttaag accccttggt 960
gaaatgggac agttggcagc ggctctgatg agcccgagaa gaggcctgcc cttgggtgag 1020
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aggcatctgt ctttgcattg gagcaggcca aggttgaggg gaaaagttaa gttaaagtgc 1380
gttctcttct atagcaaac gtattgtctg acattcagcc agcttttttt tttcttaata 1440
attctgtgca cttctgttcc ogtatttact gtatttagaa aaagcagcta gaatatttct 1500

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145/175

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gaggagtagt acgtttatct agattttctc tagataatgc aggcggaaga cctgggttcc 1620
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cagcagctct gagggcagct caatgaaaaa gtgaatgcac acgcccttgt tggcgtggcc 2880
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ccaagaaaaga tgatttttag aacctttgcc tatattaggt tgtacttatg tacatatatt 3000
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taaacatgtg ttttaatac 3078

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<210> 126

<211> 298

<212> PRT

<213> Homo sapiens

<400> 126

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Met Asn Asp Ser Leu Arg Thr Asp Val Phe Val Arg Phe Gln Pro Glu
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Ser Ile Ala Cys Ala Cys Ile Tyr Leu Ala Ala Arg Thr Leu Glu Ile
          20             25             30
Pro Leu Pro Asn Arg Pro His Trp Phe Leu Leu Phe Gly Ala Thr Glu
          35             40             45
Glu Glu Ile Gln Glu Ile Cys Leu Lys Ile Leu Gln Leu Tyr Ala Arg
          50             55             60
Lys Lys Val Asp Leu Thr His Leu Glu Gly Glu Val Glu Lys Arg Lys
          65             70             75             80
His Ala Ile Glu Glu Ala Lys Ala Gln Ala Arg Gly Leu Leu Pro Gly
          85             90             95
Gly Thr Gln Val Leu Asp Gly Thr Ser Gly Phe Ser Pro Ala Pro Lys

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100										105					110				
Leu	Val	Glu	Ser	Pro	Lys	Glu	Gly	Lys	Gly	Ser	Lys	Pro	Ser	Pro	Leu				
115										120					125				
Ser	Val	Lys	Asn	Thr	Lys	Arg	Arg	Leu	Glu	Gly	Ala	Lys	Lys	Ala	Lys				
130										135					140				
Ala	Asp	Ser	Pro	Val	Asn	Gly	Leu	Pro	Lys	Gly	Arg	Glu	Ser	Arg	Ser				
145										150					155				
Arg	Ser	Arg	Ser	Arg	Glu	Gln	Ser	Tyr	Ser	Arg	Ser	Pro	Ser	Arg	Ser				
165										170					175				
Ala	Ser	Pro	Lys	Arg	Arg	Lys	Ser	Asp	Ser	Gly	Ser	Thr	Ser	Gly	Gly				
180										185					190				
Ser	Lys	Ser	Gln	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Asp	Ser	Pro	Pro	Arg				
195										200					205				
Gln	Ala	Pro	Arg	Ser	Ala	Pro	Tyr	Lys	Gly	Ser	Glu	Ile	Arg	Gly	Ser				
210										215					220				
Arg	Lys	Ser	Lys	Asp	Cys	Lys	Tyr	Pro	Gln	Lys	Pro	His	Lys	Ser	Arg				
225										230					235				
Ser	Arg	Ser	Ser	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Glu	Arg	Ala	Asp				
245										250					255				
Asn	Pro	Gly	Lys	Tyr	Lys	Lys	Lys	Ser	His	Tyr	Tyr	Arg	Asp	Gln	Arg				
260										265					270				
Arg	Glu	Arg	Ser	Arg	Ser	Tyr	Glu	Arg	Thr	Gly	Arg	Arg	Tyr	Glu	Arg				
275										280					285				
Asp	His	Pro	Gly	His	Ser	Arg	His	Arg	Arg										
290										295									

<210> 127
 <211> 1844
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (401)..(1456)

<400> 127						
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cgcgcgggccc	gccctccccg	gogcggggct	cctctccgcg	ccctgtcgg	cgcggaaccc	180
tggcctcgtc	cgcgcccag	ctccctggag	cctcgcac	gcgggggcgc	ccccgcgagc	240
tgcgtctcc	ccggccggag	cgctcctcct	ccagcccca	gcccgcaggg	tactttgccc	300
tgggagcgaa	ggaggctcca	gaactggtag	agccgggcca	tgggctggg	cacctccccg	360
gggcgcgcgc	agcgcggagt	ccactgaccg	gctcaaaggt	atggcgttga	cggtggatgt	420
ggccggggcca	gcgccctggg	gcttcgtat	cacagggggc	agggatttcc	acacgcccac	480
catggtgact	aagggtggcg	agcggggcaa	agccaaggac	gctgacctcc	ggcctggaga	540
cataatcgtg	gccatcaacg	gggaaagcgc	ggagggcacg	ctgcatgccg	aggcccagag	600
caagatccgc	cagagccct	cgccctgcg	gctgcagctg	gaccggtctc	aggctacgtc	660

147/175

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tccagggcag accaatgggg acagctcctt ggaagtgtctg gcgactcgct tccagggctc 720
cgtgaggaca tacactgaga gtcagtccctc ctttaagggtcc tcctactcca gcccaacctc 780
cctcagcccg agggccggca gcccttctc accaccaccc tctagcagct cctcacttg 840
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tgaccgcctg tcctactcag gccgccctgg aagccgacag gccggcctcg gccgcgctgg 960
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ccagtccctc ctgcccgcct ccagggccct ggccacccct cccaagctcc acacttggtga 1260
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cgaacacaga agtgggaagg agaggggtgg gccaggggct aatgggtgtca ctgtgtaaag 1800
tttttgacat actagctcta taaatatatg aatatggaca aaat 1844

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<210> 128

<211> 352

<212> PRT

<213> Homo sapiens

<400> 128

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Met Ala Leu Thr Val Asp Val Ala Gly Pro Ala Pro Trp Gly Phe Arg
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Ile Thr Gly Gly Arg Asp Phe His Thr Pro Ile Met Val Thr Lys Val
      20             25             30
Ala Glu Arg Gly Lys Ala Lys Asp Ala Asp Leu Arg Pro Gly Asp Ile
      35             40             45
Ile Val Ala Ile Asn Gly Glu Ser Ala Glu Gly Met Leu His Ala Glu
      50             55             60
Ala Gln Ser Lys Ile Arg Gln Ser Pro Ser Pro Leu Arg Leu Gln Leu
      65             70             75             80
Asp Arg Ser Gln Ala Thr Ser Pro Gly Gln Thr Asn Gly Asp Ser Ser
      85             90             95
Leu Glu Val Leu Ala Thr Arg Phe Gln Gly Ser Val Arg Thr Tyr Thr
      100             105             110
Glu Ser Gln Ser Ser Leu Arg Ser Ser Tyr Ser Ser Pro Thr Ser Leu
      115             120             125
Ser Pro Arg Ala Gly Ser Pro Phe Ser Pro Pro Pro Ser Ser Ser Ser
      130             135             140
Leu Thr Gly Glu Ala Ala Ile Ser Arg Ser Phe Gln Ser Leu Ala Cys
      145             150             155             160

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148/175

Ser Pro Gly Leu Pro Ala Ala Asp Arg Leu Ser Tyr Ser Gly Arg Pro
 165 170 175
 Gly Ser Arg Gln Ala Gly Leu Gly Arg Ala Gly Asp Ser Ala Val Leu
 180 185 190
 Val Leu Pro Pro Ser Pro Gly Pro Arg Ser Ser Arg Pro Ser Met Asp
 195 200 205
 Ser Glu Gly Gly Ser Leu Leu Leu Asp Glu Asp Ser Glu Val Phe Lys
 210 215 220
 Met Leu Gln Glu Asn Arg Glu Gly Arg Ala Ala Pro Arg Gln Ser Ser
 225 230 235 240
 Ser Phe Arg Leu Leu Gln Glu Ala Leu Glu Ala Glu Glu Arg Gly Gly
 245 250 255
 Thr Pro Ala Phe Leu Pro Ser Ser Leu Ser Pro Gln Ser Ser Leu Pro
 260 265 270
 Ala Ser Arg Ala Leu Ala Thr Pro Pro Lys Leu His Thr Cys Glu Lys
 275 280 285
 Cys Ser Thr Ser Ile Ala Asn Gln Ala Val Arg Ile Gln Glu Gly Arg
 290 295 300
 Tyr Arg His Pro Gly Cys Tyr Thr Cys Ala Asp Cys Gly Leu Asn Leu
 305 310 315 320
 Lys Met Arg Gly His Phe Trp Val Gly Asp Glu Leu Tyr Cys Glu Lys
 325 330 335
 His Ala Arg Gln Arg Tyr Ser Ala Pro Ala Thr Leu Ser Ser Arg Ala
 340 345 350

<210> 129

<211> 2356

<212> DNA

<213> Homo sapiens

<400> 129

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 gtaattcttc ctctataaag aataggtata ggaaagactg aataaaaatg gagggatata 120
 cccttggatt tcacttgcac tgtgcaataa gcaaagaagg gttgataaaa gttcttgatc 180
 aaaaagttca aagaaaccag aatttttagac agcaagctaa ataaatattg taaaattgca 240
 ctatattagg ttaagtatta tttaggtatt ataatatgct ttgtaaattt tatattccaa 300
 atattgctca atatttttca totattaaat taattttctag tgtaaataag tagcttctat 360
 atcigtctta gtctattata attgtaagga gtaaaattaa atgaatagtc tgcaggtata 420
 aatttgaaca atgcatagat gatcgaaaat tacggaaaat catagggcag agaggtgtga 480
 agattcatca ttatgtgaaa tttaggatott totcaaatcc ttgctgaaat ttaggatggt 540
 tctcactgtt tttctgtgct gatagtaccc ttccaaaggt gaccttcagg gggattaacc 600
 ttcttagctc aagcaatgag ctaaaaggag ctttatgcat gatottccca catatcaaaa 660
 taactaaaag goactgagtt tggcattttt ctgocgtgctc tgotaagacc tttttttttt 720
 ttacttttca ttataacata ttatacatga cattatacaa aaatgattaa aatatattaa 780
 aacaacatca acaatccagg atatttttct ataaaacttt ttaaaaaataa ttgtatctat 840
 atattcaatt ttacatcctt cttcaaaggc ttgttttttc taaaggcttt gttttccttt 900
 ttattatttt tttctttttt atttttttga gacagtcttg ctctgtcgtc caggctggag 960

149/175

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tgcagtggca cgatctcagc tcaactgcaac ctctctctcc caggttcaag tgattcttgt 1020
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gtacttttag tagagacagg gtttcaccac attgggtcagg ctgggtcttga aatgctggcg 1140
tcaagtgatc tgcctgcctc cgccctcaca agcactggga ttacaggcat gaatctggcc 1200
ttacgtaata tattttctta atggctgcat aatatcacat caaataggca tttttcaaac 1260
ctctttcctt attaaacatg tagactatat ccatttttta ctaaaataaa taacatttca 1320
gataatatct ttgcaatgat aatgttgcca agccatttct aaagtgcctt tatcaattta 1380
attaccattg gatgagggtg ttgctttcat cgcaccattg taaattgtct tttttatttc 1440
aatttgctt tattttataac tggttgcaaa ggtacacaga acacacgctc cttcaactta 1500
tctttgataa acccaagcaa ggatacaaaa agttggacga cattgagtag agtcatggta 1560
tacgggtgctg accctacagt atcagtggaa aagataagga aaatgtcact actcacctat 1620
gttatgcaaa acagttaggt gtgctggggc tggatactgc tcttttactt gagcatttgt 1680
tgattaaagt ttaggtacca tccaggctgg tctagagaag tctttggagt taacctgct 1740
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gaaaatgcca tccataggta aaatgctgac ctatagaaaa aaatgaactc tacttttata 1860
gcctagtaaa aatgctctac ctgagtagtt aaaagcaatt catgaagcct gaagctaaag 1920
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aaacttcttt actgctgata tgttctgt attctagaaa aatttttaca ctttcacatt 2280
atttttgtac actttcccca tgtaaggga tgatggcttt tataaatgtg tattcattaa 2340
atgttacttt aaaaat                                     2356

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<210> 130
 <211> 1731
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (72).. (1373)

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<400> 130
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agaagatccc cgaactacgg cgacgaggcc tgcctgtggc tcgogttgct gatgccatcc 180
cttactgctc ctgagactgg gcgcttctga gggaggaaga aaaggagaaa taocgagaaa 240
tggctcgaga atggagggcc gctcagggaa aggaccctgg gccctcagag aagcagaaac 300
ctgttttcac accactgagg aggccaggca tgcttgtacc aaagcagaat gtttcacctc 360
cagatatgtc agctttgtct ttaaaagggt atcaagctct ccttggaggc attttttatt 420
ttttgaacat ttttagccat ggcgagctac ctctctattg tgaacagcgc ttctctcctt 480
gtgaaatttg ctgtgttaag tattctctcc aagaagggtat tatggcagat ttccacagtt 540
ttataaatcc tggtgaaatt ccacgaggat ttogatttca ttgtcaggct gcaagtgtatt 600
ctagtcacaa gatttctatt tcaaattttg aacgtgggca taaccaagca actgtgttac 660
aaaaccttta tagatttatt catcccaacc cagggaactg gccacctato tactgcaagt 720

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150/175

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ctgatgatag aaccagagtc aactgggtgtt tgaagcatat ggcaaaggca tcagaaatca 780
ggcaagatct acaacttctc actgtagagg accttgtagt ggggatctac caacaaaaat 840
ttctcaagga gccctctaag acttgggattc gaagcctcct agatgtggcc atgtggggatt 900
attctagcaa cacaaggtgc aagtggcatg aagaaaatga tattctcttc tgtgctttag 960
ctgtttgcaa gaagattgog tactgcatca gtaattctct ggccactctc ttiggaatcc 1020
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ctcatttcaa ctcttcta at gaggaacaaa gatcaaacac acccattggt gactacccat 1200
ctagggcaaa aatttctggc caaaacagca gcgttcgggg aagaggaatt acccgcttac 1260
tagagagcat ttccaattct tccagcaata tccacaaaatt ctccaactgt gacacttcac 1320
tctcaacctta catgtcccaa aaagatggat acaaattctt ctcttcctta tcttaatgat 1380
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tttcttgagg gattgttctg cttcctggct gtatgatggg tatatcatta aagtttggag 1620
tcctatatga acaaaactga cttttttaga gttgtacttt tgggaatgtt atagattgat 1680
cattctttct cctgataata aaggtattga atatctgita tgaaaggttc t 1731

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<210> 131

<211> 434

<212> PRT

<213> Homo sapiens

<400> 131

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Met Pro Asn Arg Lys Ala Ser Arg Asn Ala Tyr Tyr Phe Phe Val Gln
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Glu Lys Ile Pro Glu Leu Arg Arg Arg Gly Leu Pro Val Ala Arg Val
             20             25             30
Ala Asp Ala Ile Pro Tyr Cys Ser Ser Asp Trp Ala Leu Leu Arg Glu
             35             40             45
Glu Glu Lys Glu Lys Tyr Ala Glu Met Ala Arg Glu Trp Arg Ala Ala
             50             55             60
Gln Gly Lys Asp Pro Gly Pro Ser Glu Lys Gln Lys Pro Val Phe Thr
             65             70             75             80
Pro Leu Arg Arg Pro Gly Met Leu Val Pro Lys Gln Asn Val Ser Pro
             85             90             95
Pro Asp Met Ser Ala Leu Ser Leu Lys Gly Asp Gln Ala Leu Leu Gly
             100            105            110
Gly Ile Phe Tyr Phe Leu Asn Ile Phe Ser His Gly Glu Leu Pro Pro
             115            120            125
His Cys Glu Gln Arg Phe Leu Pro Cys Glu Ile Gly Cys Val Lys Tyr
             130            135            140
Ser Leu Gln Glu Gly Ile Met Ala Asp Phe His Ser Phe Ile Asn Pro
             145            150            155            160
Gly Glu Ile Pro Arg Gly Phe Arg Phe His Cys Gln Ala Ala Ser Asp
             165            170            175
Ser Ser His Lys Ile Pro Ile Ser Asn Phe Glu Arg Gly His Asn Gln

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151/175

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Ala	Thr	Val	Leu	Gln	Asn	Leu	Tyr	Arg	Phe	Ile	His	Pro	Asn	Pro	Gly									
		195					200					205												
Asn	Trp	Pro	Pro	Ile	Tyr	Cys	Lys	Ser	Asp	Asp	Arg	Thr	Arg	Val	Asn									
		210					215					220												
Trp	Cys	Leu	Lys	His	Met	Ala	Lys	Ala	Ser	Glu	Ile	Arg	Gln	Asp	Leu									
		225			230					235					240									
Gln	Leu	Leu	Thr	Val	Glu	Asp	Leu	Val	Val	Gly	Ile	Tyr	Gln	Gln	Lys									
				245					250					255										
Phe	Leu	Lys	Glu	Pro	Ser	Lys	Thr	Trp	Ile	Arg	Ser	Leu	Leu	Asp	Val									
		260					265					270												
Ala	Met	Trp	Asp	Tyr	Ser	Ser	Asn	Thr	Arg	Cys	Lys	Trp	His	Glu	Glu									
		275					280					285												
Asn	Asp	Ile	Leu	Phe	Cys	Ala	Leu	Ala	Val	Cys	Lys	Lys	Ile	Ala	Tyr									
		290					295					300												
Cys	Ile	Ser	Asn	Ser	Leu	Ala	Thr	Leu	Phe	Gly	Ile	Gln	Leu	Thr	Glu									
		305			310					315					320									
Ala	His	Val	Pro	Leu	Gln	Asp	Tyr	Glu	Ala	Ser	Asn	Ser	Val	Thr	Pro									
				325					330					335										
Lys	Met	Val	Val	Leu	Asp	Ala	Gly	Arg	Tyr	Gln	Lys	Leu	Arg	Val	Gly									
		340					345					350												
Ser	Ser	Gly	Phe	Ser	His	Phe	Asn	Ser	Ser	Asn	Glu	Glu	Gln	Arg	Ser									
		355					360					365												
Asn	Thr	Pro	Ile	Gly	Asp	Tyr	Pro	Ser	Arg	Ala	Lys	Ile	Ser	Gly	Gln									
		370					375					380												
Asn	Ser	Ser	Val	Arg	Gly	Arg	Gly	Ile	Thr	Arg	Leu	Leu	Glu	Ser	Ile									
		385			390					395					400									
Ser	Asn	Ser	Ser	Ser	Asn	Ile	His	Lys	Phe	Ser	Asn	Cys	Asp	Thr	Ser									
				405					410					415										
Leu	Ser	Pro	Tyr	Met	Ser	Gln	Lys	Asp	Gly	Tyr	Lys	Ser	Phe	Ser	Ser									
				420					425					430										
Leu	Ser																							

<210> 132

<211> 1561

〈212〉 DNA

〈213〉 *Homo sapiens*

<220>

<221> CDS

<222> (385) . . (1281)

<400> 132

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ctgcagcacc tgaaggaacc atctggggcct tcagagotta ttccctoaaag taccttcagt 120
gcacacaaca ggagagagga gaaagaagaa acgctagtaa ttccaagcac tggaattaag 180

152/175

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gattttgact ttgatgatcc agataatctg cttgaggatg actttattct tcaggccaat 360
aaggcaacag gagaggaaga gggaatggat atacagaaat ctgagaatga agatgacagc 420
gagtgggaag atgtggatga tgagaaggga gatagcaatg atgactatga ctctgcaggc 480
ctattgtcag atgaagactg tatgtctgtg ccgggaaaaa ctcacagagc tatagcagat 540
cacttgttct ggagtgagga aacaaagagt cgcttcacgg agtattcgat gacttcctca 600
gtcatgagga gaaatgaaca gctgacccta catgatgaga ggtttgagaa gttttatgag 660
caatatgatg atgatgaaat tggagctctg gataatgcag aattggaagg ttctattcaa 720
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gatgagtctg aggaggaaga aatgattact gtagtccttg aagaagccaa agagaagtgg 900
gatttgtaat ctattttag tagataactca aatttatata accatccaca gcttatcaag 960
tatcaaccaa agcccaaaca aattcgaata tcttctaaaa caggaatacc tctcaatgtc 1020
ttaccaaaaga aaggactcac agcaaagcaa actgaaagaa tacagatgat taatggcagt 1080
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aaattagcat ttaaactgga gaaaagaagg caagaaaaag agctgctgaa cttgaagaag 1260
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gctctcctac tttggttatt gactagaaac ttcagaaaga caaaactgtt tgccattttt 1380
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gccaaccatc ttgtaaatat tgtaatactt taatttttaa tattataagc ttacatttgc 1500
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<210> 133

<211> 299

<212> PRT

<213> Homo sapiens

<400> 133

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Met Asp Ile Gln Lys Ser Glu Asn Glu Asp Asp Ser Glu Trp Glu Asp
  1             5             10             15
Val Asp Asp Glu Lys Gly Asp Ser Asn Asp Asp Tyr Asp Ser Ala Gly
          20             25             30
Leu Leu Ser Asp Glu Asp Cys Met Ser Val Pro Gly Lys Thr His Arg
          35             40             45
Ala Ile Ala Asp His Leu Phe Trp Ser Glu Glu Thr Lys Ser Arg Phe
          50             55             60
Thr Glu Tyr Ser Met Thr Ser Ser Val Met Arg Arg Asn Glu Gln Leu
          65             70             75             80
Thr Leu His Asp Glu Arg Phe Glu Lys Phe Tyr Glu Gln Tyr Asp Asp
          85             90             95
Asp Glu Ile Gly Ala Leu Asp Asn Ala Glu Leu Glu Gly Ser Ile Gln
          100             105             110
Val Asp Ser Asn Arg Leu Gln Glu Val Leu Asn Asp Tyr Tyr Lys Glu
          115             120             125

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153/175

Lys Ala Glu Asn Cys Val Lys Leu Asn Thr Leu Glu Pro Leu Glu Asp
 130 135 140
 Gln Asp Leu Pro Met Asn Glu Leu Asp Glu Ser Glu Glu Glu Glu Met
 145 150 155 160
 Ile Thr Val Val Leu Glu Glu Ala Lys Glu Lys Trp Asp Cys Glu Ser
 165 170 175
 Ile Cys Ser Thr Tyr Ser Asn Leu Tyr Asn His Pro Gln Leu Ile Lys
 180 185 190
 Tyr Gln Pro Lys Pro Lys Gln Ile Arg Ile Ser Ser Lys Thr Gly Ile
 195 200 205
 Pro Leu Asn Val Leu Pro Lys Lys Gly Leu Thr Ala Lys Gln Thr Glu
 210 215 220
 Arg Ile Gln Met Ile Asn Gly Ser Asp Leu Pro Lys Val Ser Thr Gln
 225 230 235 240
 Pro Arg Ser Lys Asn Glu Ser Lys Glu Asp Lys Arg Ala Arg Lys Gln
 245 250 255
 Ala Ile Lys Glu Glu Arg Lys Glu Arg Arg Val Glu Lys Lys Ala Asn
 260 265 270
 Lys Leu Ala Phe Lys Leu Glu Lys Arg Arg Gln Glu Lys Glu Leu Leu
 275 280 285
 Asn Leu Lys Lys Asn Val Glu Gly Leu Lys Leu
 290 295

<210> 134

<211> 2497

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (305).. (970)

<400> 134

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 tcgctcctcc ctgcggaccc tggggtcagt gggagagccc atcaactgtg aggcctggga 180
 gtggcttcac aggggtggtgg gggacagcag gtgcacgctg gtggacacct ggtggcagac 240
 agaaacaggt ggcattctgca tcgcaccacg gccctcggaa gaaggggagg aaatcctccc 300
 tgccatggcg atgaggccct tctttggcat cgtccccgtc ctcatggatg agaagggcag 360
 cgtcgtggag ggcagcaacg tctccggggc cctgtgcatc tcccaggcct ggccgggcat 420
 ggccaggacc atctatggcg accaccagcg atttgtggac gcctacttca aggcctaccc 480
 aggcatttac ttactggag acggggctta ccgaactgag ggcggtatt accagatcac 540
 agggcgggatg gatgatgtca tcaacatcag tggccaccgg ctggggaccg cagagattga 600
 ggacgccatc gccgaccacc ctgcagtacc agaaagtgtc gtcattggct acccccacga 660
 catcaaagga gaagctgcct ttgccttcac tgttggtgaaa gatagtgcgg gtgaactcaga 720
 tgttggtggtg caggagctca agtccatggt ggccaccaag atcgccaaat atgctgtgcc 780
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154/175

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tgctgctaag tgagctggca ccttggtggg ctcttgggat gggcgggcac ccaagccctg 1020
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cccaccccac acatgaccca caccgccctc acgtgaagct gggctgagag ccctttctcc 1140
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ggttctgcca tctgagtttg gtttcctgga atgaaaaggc attgccatct ccattcctct 1260
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gaaatcttat ttttatactt ttatatgtg gaagaacagc atgcaacact cacatgtagt 1440
gtgtggattt acttgaacat gttcttttta acatgtagtt atgaaaatct ccttttttgc 1500
ctctactggg gaggaacat gaggatcaga gccacattt ttaattattg ttagtgatt 1560
tggaagtctg aattggagat gtttgtacct ctgtctaaac agttcccttg agaacttcca 1620
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tgtggttggg gcagtgagaa ccaactgaggt ccaatgatga gacttggagg totggatcca 1980
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cgacgccagt ggggtgcttac ctccctgcta ggcattgcagg ggctggcggg tggcagggga 2100
aggaggccca gtgagccggg tcccttaggg gagggagagt ttgtctctt tgcacacag 2160
tctacccttc agggccttgt ggcagtgcc gtgttcgggg ggtgtctggg ccactgagta 2220
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gcttagcttt ccatgttgct gagaggaacc tggacatggt cccgggcato tgaatgatct 2460
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<210> 135

<211> 222

<212> PRT

<213> Homo sapiens

<400> 135

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Met Ala Met Arg Pro Phe Phe Gly Ile Val Pro Val Leu Met Asp Glu
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Lys Gly Ser Val Val Glu Gly Ser Asn Val Ser Gly Ala Leu Cys Ile
          20             25             30
Ser Gln Ala Trp Pro Gly Met Ala Arg Thr Ile Tyr Gly Asp His Gln
          35             40             45
Arg Phe Val Asp Ala Tyr Phe Lys Ala Tyr Pro Gly Tyr Tyr Phe Thr
          50             55             60
Gly Asp Gly Ala Tyr Arg Thr Glu Gly Gly Tyr Tyr Gln Ile Thr Gly
          65             70             75             80
Arg Met Asp Asp Val Ile Asn Ile Ser Gly His Arg Leu Gly Thr Ala
          85             90             95

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155/175

Glu Ile Glu Asp Ala Ile Ala Asp His Pro Ala Val Pro Glu Ser Ala
 100 105 110
 Val Ile Gly Tyr Pro His Asp Ile Lys Gly Glu Ala Ala Phe Ala Phe
 115 120 125
 Ile Val Val Lys Asp Ser Ala Gly Asp Ser Asp Val Val Val Gln Glu
 130 135 140
 Leu Lys Ser Met Val Ala Thr Lys Ile Ala Lys Tyr Ala Val Pro Asp
 145 150 155 160
 Glu Ile Leu Val Val Lys Arg Leu Pro Lys Thr Arg Ser Gly Lys Val
 165 170 175
 Met Arg Arg Leu Leu Arg Lys Ile Ile Thr Ser Glu Ala Gln Glu Leu
 180 185 190
 Gly Asp Thr Thr Thr Leu Glu Asp Pro Ser Ile Ile Ala Glu Ile Leu
 195 200 205
 Ser Val Tyr Gln Lys Cys Lys Asp Lys Gln Ala Ala Ala Lys
 210 215 220

<210> 136

<211> 1972

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (666).. (1487)

<400> 136

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 acggcgaggc cgggccccca gccccgagcc ccgcgcccgg cccgcccgtc aaggaggagc 180
 ccgcgctgcc ctccggcgcc ggccccctgc ccgaccgcgc cccggccccg ccgcccccg 240
 ccgaggggcg ctaccggggac gagcagattt acagcgccag cgtcacgggc ctctactgga 300
 agctgcttcc ggagcaggct gcgcccccg gcgcagggga ccccggggag gggggctgtg 360
 gccggcgctg gcggggcgac cgcgtaacgg tgctgctggc cgcaaacctg accggcagcc 420
 acaagctgaa gccgctggtc atcgggcggc tgccggaccc gccagcctg cgccaccaca 480
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 tgctgcgggg ctggttcttt gaggaatttg tcccaggcgt caaacgctac ctgcgccgaa 600
 gctgcctgca gcagaaggcc gtgctgctgg tggcccaccc gccctgcca agcccagctg 660
 ccagtatgcc cggcctggac agcgaggatg ccccgctgcg gtgcaggccg gagcccctcg 720
 gtcccccgga ggagctgcag acaccggatg gcgctgtgcg ggtgctgttc ctgtccaaag 780
 gcagcagccg ggcacatata cccgcaccgc tggagcaggg cgtggtggcc gccttcaaac 840
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 gcttcatgcg cagcttcatg ctcaaggaca tgctctacct ggttggcctc tcctgggacc 960
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156/175

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aggaggtggg cccagccctg cccctgcag cgcctcggc cccagccagt ctgccctctg 1260
ccattggggg cggagaggac gaggaggagg ccaccgacta tggagggacc tcagtgcga 1320
ctgcggggga ggccgtgcg gggctagaaa cagctctgcg gtggctggag aaccaggacc 1380
ccagagaggt ggggcccactg aggctgtgc agttgogctc actcatcagc atggcccgga 1440
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ccagtgaact ttctcctgct gcacttggag ggaggggaca tacacacagt ctcccatctc 1560
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gctgggcctc cgcacctgca ccagtcacat gcactggaog agggccgaaa ctctgtctg 1860
ctatcgagcc ctggtgctat gtggcccgag agccacagca caatcatctc agtggcgaag 1920
cacaccactt gattctattt tttttaaca cattaaatct gttttaaag at 1972

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<210> 137

<211> 274

<212> PRT

<213> Homo sapiens

<400> 137

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Pro Leu Gly Pro Pro Glu Glu Leu Gln Thr Pro Asp Gly Ala Val Arg
      20           25           30
Val Leu Phe Leu Ser Lys Gly Ser Ser Arg Ala His Ile Pro Ala Pro
      35           40           45
Leu Glu Gln Gly Val Val Ala Ala Phe Lys Gln Leu Tyr Lys Arg Glu
      50           55           60
Leu Leu Arg Leu Ala Val Ser Cys Ala Ser Gly Ser Pro Leu Gly Phe
      65           70           75           80
Met Arg Ser Phe Met Leu Lys Asp Met Leu Tyr Leu Ala Gly Leu Ser
      85           90           95
Trp Asp Leu Val Gln Ala Gly Ser Ile Glu Arg Cys Trp Leu Leu Gly
      100          105          110
Leu Arg Ala Ala Phe Glu Pro Arg Pro Gly Glu Asp Ser Ala Gly Gln
      115          120          125
Pro Ala Gln Ala Glu Glu Ala Ala Glu His Ser Arg Val Leu Ser Asp
      130          135          140
Leu Thr His Leu Ala Ala Leu Ala Tyr Lys Cys Leu Ala Pro Glu Glu
      145          150          155          160
Val Ala Glu Trp Leu His Leu Asp Asp Asp Gly Gly Pro Pro Glu Gly
      165          170          175
Cys Arg Glu Glu Val Gly Pro Ala Leu Pro Pro Ala Ala Pro Pro Ala
      180          185          190
Pro Ala Ser Leu Pro Ser Ala Ile Gly Gly Gly Glu Asp Glu Glu Glu
      195          200          205
Ala Thr Asp Tyr Gly Gly Thr Ser Val Pro Thr Ala Gly Glu Ala Val

```


157/175

210	215	220
Arg Gly Leu Glu Thr Ala Leu Arg Trp Leu Glu Asn Gln Asp Pro Arg		
225	230	235
Glu Val Gly Pro Leu Arg Leu Val Gln Leu Arg Ser Leu Ile Ser Met		240
	245	250
Ala Arg Arg Leu Gly Gly Ile Gly His Thr Pro Ala Gly Pro Tyr Asp		255
	260	265
		270
Gly Val		

<210> 138
 <211> 3677
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (996).. (3437)

<400> 138
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 tcaaacgctc agacatgctg agggatgtca tccgagaata tgatgaatat ttcccagaaa 180
 tcattgaacg agcaagctac actctggaga agatgtttcg agtcaatctg aaagaaattg 240
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 tgaatggcaa caaggcgggt gaggctgtca tctgggagggt gctgcgcaag ttggggctgc 420
 gccctgggta tgactgggct ctctcagcgc ttgctgtccg tgttgtcctt tggcaagaga 480
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 gcttcagcag cgcagccagc attagotitg gttgtgcaca cagcaccagc actagtttca 1560
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158/175

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gcaccagctt tggcagtga cccacaacga gcacagtctt cagtagtgcg cttagcacca 1800
gcactggctt tggaggcata ctcagcacca gtgtctgttt tggtaggctct cccagctcca 1860
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attaaatttg caaatg 3677

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<210> 139

<211> 814

<212> PRT

<213> Homo sapiens

<400> 139

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Met Lys Val Leu Lys Phe Ala Cys Arg Val Gln Lys Lys Asp Pro Lys
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Asp Trp Ala Val Gln Tyr Arg Glu Ala Val Glu Met Glu Val Gln Ala
          20             25             30
Ala Ala Val Ala Val Ala Glu Ala Glu Ala Arg Ala Glu Ala Arg Ala

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		35					40				45				
Gln	Met	Gly	Ile	Gly	Glu	Glu	Ala	Val	Ala	Gly	Pro	Trp	Asn	Trp	Asp
	50					55					60				
Asp	Met	Asp	Ile	Asp	Cys	Leu	Thr	Arg	Glu	Glu	Leu	Gly	Asp	Asp	Ala
65					70					75					80
Gln	Ala	Trp	Ser	Arg	Phe	Ser	Phe	Glu	Ile	Glu	Ala	Arg	Ala	Gln	Glu
				85					90					95	
Asn	Ala	Asp	Ala	Ser	Thr	Asn	Val	Asn	Phe	Ser	Arg	Gly	Ala	Ser	Thr
			100					105					110		
Arg	Ala	Gly	Phe	Ser	Asp	Gly	Ala	Ser	Ile	Ser	Phe	Asn	Gly	Ala	Pro
		115					120					125			
Ser	Ser	Ser	Gly	Gly	Phe	Ser	Gly	Gly	Pro	Gly	Ile	Thr	Phe	Gly	Val
		130				135					140				
Ala	Pro	Ser	Thr	Ser	Ala	Ser	Phe	Ser	Asn	Thr	Ala	Ser	Ile	Ser	Phe
145					150					155					160
Gly	Gly	Thr	Leu	Ser	Thr	Ser	Ser	Ser	Phe	Ser	Ser	Ala	Ala	Ser	Ile
				165					170					175	
Ser	Phe	Gly	Cys	Ala	His	Ser	Thr	Ser	Thr	Ser	Phe	Ser	Ser	Glu	Ala
			180					185					190		
Ser	Ile	Ser	Phe	Gly	Gly	Met	Pro	Cys	Thr	Ser	Ala	Ser	Phe	Ser	Gly
		195				200					205				
Gly	Val	Ser	Ser	Ser	Phe	Ser	Gly	Pro	Leu	Ser	Thr	Ser	Ala	Thr	Phe
	210					215					220				
Ser	Gly	Gly	Ala	Ser	Ser	Gly	Phe	Gly	Gly	Thr	Leu	Ser	Thr	Thr	Ala
225					230					235					240
Gly	Phe	Ser	Gly	Val	Leu	Ser	Thr	Ser	Thr	Ser	Phe	Gly	Ser	Ala	Pro
				245					250					255	
Thr	Thr	Ser	Thr	Val	Phe	Ser	Ser	Ala	Leu	Ser	Thr	Ser	Thr	Gly	Phe
			260					265					270		
Gly	Gly	Ile	Leu	Ser	Thr	Ser	Val	Cys	Phe	Gly	Gly	Ser	Pro	Ser	Ser
		275				280						285			
Ser	Gly	Ser	Phe	Gly	Gly	Thr	Leu	Ser	Thr	Ser	Ile	Cys	Phe	Gly	Gly
	290					295				300					
Ser	Pro	Cys	Thr	Ser	Thr	Gly	Phe	Gly	Gly	Thr	Leu	Ser	Thr	Ser	Val
305					310					315					320
Ser	Phe	Gly	Gly	Ser	Ser	Ser	Thr	Ser	Ala	Asn	Phe	Gly	Gly	Thr	Leu
				325					330					335	
Ser	Thr	Ser	Ile	Cys	Phe	Asp	Gly	Ser	Pro	Ser	Thr	Gly	Ala	Gly	Phe
			340					345					350		
Gly	Gly	Ala	Leu	Asn	Thr	Ser	Ala	Ser	Phe	Gly	Ser	Val	Leu	Asn	Thr
		355					360					365			
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	370					375					380			</	

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161/175

805

810

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162/175

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163/175

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<210> 141
 <211> 613
 <212> PRT
 <213> Homo sapiens

<400> 141

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Val	Ser	Lys	Ala	Lys	His	Leu	Gln	Phe	Phe	Ser	Gly	Val	Lys	Pro	Val	35	40	45	
Ile	Tyr	Trp	Leu	Ser	Asn	Phe	Val	Trp	Asp	Met	Cys	Asn	Tyr	Val	Val	50	55	60	
Pro	Ala	Thr	Leu	Val	Ile	Ile	Ile	Phe	Ile	Cys	Phe	Gln	Gln	Lys	Ser	65	70	75	80
Tyr	Val	Ser	Ser	Thr	Asn	Leu	Pro	Val	Leu	Ala	Leu	Leu	Leu	Leu	Leu	85	90	95	
Tyr	Gly	Trp	Ser	Ile	Thr	Pro	Leu	Met	Tyr	Pro	Ala	Ser	Phe	Val	Phe	100	105	110	
Lys	Ile	Pro	Ser	Thr	Ala	Tyr	Val	Val	Leu	Thr	Ser	Val	Asn	Leu	Phe	115	120	125	
Ile	Gly	Ile	Asn	Gly	Ser	Val	Ala	Thr	Phe	Val	Leu	Glu	Leu	Phe	Thr	130	135	140	
Asp	Asn	Lys	Leu	Asn	Asn	Ile	Asn	Asp	Ile	Leu	Lys	Ser	Val	Phe	Leu	145	150	155	160
Ile	Phe	Pro	His	Phe	Cys	Leu	Gly	Arg	Gly	Leu	Ile	Asp	Met	Val	Lys	165	170	175	
Asn	Gln	Ala	Met	Ala	Asp	Ala	Leu	Glu	Arg	Phe	Gly	Glu	Asn	Arg	Phe	180	185	190	
Val	Ser	Pro	Leu	Ser	Trp	Asp	Leu	Val	Gly	Arg	Asn	Leu	Phe	Ala	Met	195	200	205	
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Tyr	Arg	Arg	Lys	Arg	Lys	Pro	Ala	Val	Asp	Arg	Ile	Cys	Val	Gly	Ile	275	280	285	
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164/175

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 Pro Glu Lys Glu Val Gly Lys Val Gly Glu Trp Ala Ile Arg Lys Leu
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 Gly Leu Val Lys Tyr Gly Glu Lys Tyr Ala Gly Asn Tyr Ser Gly Gly
 385 390 395 400
 Asn Lys Arg Lys Leu Ser Thr Ala Met Ala Leu Ile Gly Gly Pro Pro
 405 410 415
 Val Val Phe Leu Asp Glu Pro Thr Thr Gly Met Asp Pro Lys Ala Arg
 420 425 430
 Arg Phe Leu Trp Asn Cys Ala Leu Ser Val Val Lys Glu Gly Arg Ser
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 Val Val Leu Thr Ser His Ser Met Glu Glu Cys Glu Ala Leu Cys Thr
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 Arg Met Ala Ile Met Val Asn Gly Arg Phe Arg Cys Leu Gly Ser Val
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 Gln His Leu Lys Asn Arg Phe Gly Asp Gly Tyr Thr Ile Val Val Arg
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<211> 2214

<212> DNA

<213> Homo sapiens

<220>

165/175

<221> CDS

<222> (81).. (734)

<400> 142

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<211> 218

<212> PRT

<213> Homo sapi ns

166/175

<400> 143

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          50          55          60
Lys Val Ala Ile Ser Ala Ile Tyr Met Asp Leu Glu Ile Cys Glu Val
          65          70          75          80
Leu Glu Arg Ser His Ser Pro Pro Leu Lys Leu Thr Pro Ala Ser Ser
          85          90          95
Thr His Pro Asn Leu His Ala Tyr Leu Gln Gly Asn Thr Gln Val Ser
          100          105          110
Arg Lys Lys Leu Leu Pro Leu Leu Gln Glu Ala Leu Ser Ala Tyr Phe
          115          120          125
Asp Ser Met Lys Ile Pro Ser Gly Gln Pro Glu Thr Ala Asp Val Ser
          130          135          140
Arg Glu Gln Val Asp Lys Glu Leu Asp Arg Ala Ser Asn Ser Leu Ile
          145          150          155          160
Ser Gly Leu Ser Gln Asp Glu Glu Asp Pro Pro Leu Pro Pro Thr Pro
          165          170          175
Met Asn Ser Leu Val Asp Glu Cys Pro Leu Asp Gln Gly Leu Pro Lys
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Gln Ser Thr Thr Ala Ser Leu Ser Lys Lys
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<211> 1750

<212> DNA

<213> Homo sapiens

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<222> (158).. (1492)

<400> 144

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167/175

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<210> 145

<211> 445

<212> PRT

<213> Homo sapiens

<400> 145

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Glu Leu Pro Val Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro
  35             40             45
Ser Tyr Val Ser Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val
  50             55             60
Val Thr Leu Trp Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro
  65             70             75             80
Ile Arg Val Val Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala
  85             90             95
Ser Leu Trp His His Val Ala Pro Val Ala Gly Gln Leu His Ser Val
  100            105            110
Ala Phe Leu Ala Leu Ala Phe Val Leu Ala Leu Ala Cys Cys Ala Ser
  115            120            125
Asn Val Thr Phe Leu Pro Phe Leu Ser His Leu Pro Pro Arg Phe Leu

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168/175

130	135										140						
Arg	Ser	Phe	Phe	Leu	Gly	Gln	Gly	Leu	Ser	Ala	Leu	Leu	Pro	Cys	Val		
145	150										155					160	
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165				170										175			
Ile	Asn	Gly	Thr	Pro	Gly	Pro	Pro	Leu	Asp	Phe	Leu	Glu	Arg	Phe	Pro		
180				185										190			
Ala	Ser	Thr	Phe	Phe	Trp	Ala	Leu	Thr	Ala	Leu	Leu	Val	Ala	Ser	Ala		
195				200										205			
Ala	Ala	Phe	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Pro	Pro	Ser	Val		
210				215										220			
Pro	Thr	Gly	Glu	Leu	Gly	Ser	Gly	Leu	Gln	Val	Gly	Ala	Pro	Gly	Ala		
225	230										235					240	
Glu	Glu	Glu	Val	Glu	Gly	Ser	Ser	Pro	Leu	Gln	Glu	Pro	Pro	Ser	Gln		
245				250										255			
Ala	Ala	Gly	Thr	Thr	Pro	Gly	Pro	Asp	Pro	Lys	Ala	Tyr	Gln	Leu	Leu		
260				265										270			
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275				280										285			
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Tyr	Gly	Arg	Leu	Ala	Tyr	His	Leu	Ala	Val	Val	Leu	Gly	Ser	Ala	Ala		
305	310										315					320	
Asn	Pro	Leu	Ala	Cys	Phe	Leu	Ala	Met	Gly	Val	Leu	Cys	Arg	Ser	Leu		
325				330										335			
Ala	Gly	Leu	Gly	Gly	Leu	Ser	Leu	Leu	Gly	Val	Phe	Cys	Gly	Gly	Tyr		
340				345										350			
Leu	Met	Ala	Leu	Ala	Val	Leu	Ser	Pro	Cys	Pro	Pro	Leu	Val	Gly	Thr		
355				360										365			
Ser	Ala	Gly	Val	Val	Leu	Val	Val	Leu	Ser	Trp	Val	Leu	Cys	Leu	Gly		
370				375										380			
Val	Phe	Ser	Tyr	Val	Lys	Val	Ala	Ala	Ser	Ser	Leu	Leu	His	Gly	Gly		
385	390										395					400	
Gly	Arg	Pro	Ala	Leu	Leu	Ala	Ala	Gly	Val	Ala	Ile	Gln	Val	Gly	Ser		
405				410										415			
Leu	Leu	Gly	Ala	Val	Ala	Met	Phe	Pro	Pro	Thr	Ser	Ile	Tyr	His	Val		
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Phe	His	Ser	Arg	Lys	Asp	Cys	Ala	Asp	Pro	Cys	Asp	Ser					
435				440										445			

<210> 146

<211> 2291

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

169/175

<222> (132).. (740)

<400> 146

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atgacagaaa gatgtgtgtt ctcggactct gtgctcttat tgatatggaa cagatacccc 180
aagttttaaa tcaggtttct ggacagattt tgccggcttt tatcctttta tttaacggat 240
tgaaaagagc atatgcctgc catgcagaac atgagaatga cagtgatgat gatgatgaag 300
ctgaagatga tgatgaaacc gaggaactgg ggagtgatga agatgatatt gatgaagatg 360
ggcaagaata tttggagatt ctggctaagc aggctggtga agatggagat gatgaagatt 420
gggaagaaga tgatgctgaa gagactgctc tggaaggcta ttccacaatc attgatgatg 480
aagatacccc tgttgatgag tatcagatat ttaaagctat ctttcaaact attcaaaatc 540
gtaatcctgt gtggtatcag ggcgtgactc acggctctta tgaagaacaa agaaaacagt 600
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gcccagcacc agggatgaat tgagttatct ctttctttcc tgctgtgtgc ttgtagtga 780
gagcttgtgt tctcctagt agtggttcca gaactggttc atgttatcta ttctaaacta 840
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caaaatattt caaattgaaa gcaacatctt aatggattca aaactattac aagctgttgt 2220
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<210> 147

<211> 203

<212> PRT

<213> Homo sapiens

170/175

<400> 147

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Gln Val Leu Asn Gln Val Ser Gly Gln Ile Leu Pro Ala Phe Ile Leu
 20          25          30
Leu Phe Asn Gly Leu Lys Arg Ala Tyr Ala Cys His Ala Glu His Glu
 35          40          45
Asn Asp Ser Asp Asp Asp Asp Glu Ala Glu Asp Asp Asp Glu Thr Glu
 50          55          60
Glu Leu Gly Ser Asp Glu Asp Asp Ile Asp Glu Asp Gly Gln Glu Tyr
 65          70          75          80
Leu Glu Ile Leu Ala Lys Gln Ala Gly Glu Asp Gly Asp Asp Glu Asp
 85          90          95
Trp Glu Glu Asp Asp Ala Glu Glu Thr Ala Leu Glu Gly Tyr Ser Thr
100          105          110
Ile Ile Asp Asp Glu Asp Asn Pro Val Asp Glu Tyr Gln Ile Phe Lys
115          120          125
Ala Ile Phe Gln Thr Ile Gln Asn Arg Asn Pro Val Trp Tyr Gln Ala
130          135          140
Leu Thr His Gly Leu Asn Glu Glu Gln Arg Lys Gln Leu Gln Asp Ile
145          150          155          160
Ala Thr Leu Ala Asp Gln Arg Arg Ala Ala His Glu Ser Lys Met Ile
165          170          175
Glu Lys His Gly Gly Tyr Lys Phe Ser Ala Pro Val Val Pro Ser Ser
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<210> 148

<211> 2148

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (64).. (1812)

<400> 148

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<210> 149

<211> 583

<212> PRT

<213> Homo sapiens

<400> 149

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          20             25             30
Tyr Gln Leu Glu Leu Asp Ala Ala Val Ala Glu Val Lys Leu Arg Asp
          35             40             45
Asp Gln Tyr Thr Leu Glu His Met His Ala Phe Gly Met Tyr Asn Tyr
          50             55             60
Leu His Cys Asp Ser Trp Tyr Gln Asp Ser Val Tyr Tyr Ile Asp Thr
          65             70             75             80
Leu Gly Arg Ile Met Asn Leu Thr Val Met Leu Asp Thr Ala Leu Gly
          85             90             95

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172/175

Lys Pro Arg Glu Val Phe Arg Leu Pro Thr Asp Leu Thr Ala Cys Asp
 100 105 110
 Asn Arg Leu Cys Ala Ser Ile His Phe Ser Ser Ser Thr Trp Val Thr
 115 120 125
 Leu Ser Asp Gly Thr Gly Arg Leu Tyr Val Ile Gly Thr Gly Glu Arg
 130 135 140
 Gly Asn Ser Ala Ser Glu Lys Trp Glu Ile Met Phe Asn Glu Glu Leu
 145 150 155 160
 Gly Asp Pro Phe Ile Ile Ile His Ser Ile Ser Leu Leu Asn Ala Glu
 165 170 175
 Glu His Ser Ile Ala Thr Leu Leu Leu Arg Ile Glu Lys Glu Glu Leu
 180 185 190
 Asp Met Lys Gly Ser Gly Phe Tyr Val Ser Leu Glu Trp Val Thr Ile
 195 200 205
 Ser Lys Lys Asn Gln Asp Asn Lys Lys Tyr Glu Ile Ile Lys Arg Asp
 210 215 220
 Ile Leu Arg Gly Lys Ser Val Pro His Tyr Ala Ala Ile Glu Pro Asp
 225 230 235 240
 Gly Asn Gly Leu Met Ile Val Ser Tyr Lys Ser Leu Thr Phe Val Gln
 245 250 255
 Ala Gly Gln Asp Leu Glu Glu Asn Met Asp Glu Asp Ile Ser Glu Lys
 260 265 270
 Ile Lys Glu Pro Leu Tyr Tyr Trp Gln Gln Thr Glu Asp Asp Leu Thr
 275 280 285
 Val Thr Ile Arg Leu Pro Glu Asp Ser Thr Lys Glu Asp Ile Gln Ile
 290 295 300
 Gln Phe Leu Pro Asp His Ile Asn Ile Val Leu Lys Asp His Gln Phe
 305 310 315 320
 Leu Glu Gly Lys Leu Tyr Ser Ser Ile Asp His Glu Ser Ser Thr Trp
 325 330 335
 Ile Ile Lys Glu Ser Asn Ser Leu Glu Ile Ser Leu Ile Lys Lys Asn
 340 345 350
 Glu Gly Leu Thr Trp Pro Glu Leu Val Ile Gly Asp Lys Gln Gly Glu
 355 360 365
 Leu Ile Arg Asp Ser Ala Gln Cys Ala Ala Ile Ala Glu Arg Leu Met
 370 375 380
 His Leu Thr Ser Glu Glu Leu Asn Pro Asn Pro Asp Lys Glu Lys Pro
 385 390 395 400
 Pro Cys Ser Ala Gln Glu Leu Glu Glu Cys Asp Ile Phe Phe Glu Glu
 405 410 415
 Ser Ser Ser Leu Cys Arg Phe Asp Gly Asn Thr Leu Lys Thr Thr His
 420 425 430
 Val Val Asn Leu Gly Ser Asn Gln Tyr Leu Phe Ser Val Ile Val Asp
 435 440 445
 Pro Lys Glu Met Pro Cys Phe Cys Leu Arg His Asp Val Asp Ala Leu
 450 455 460
 Leu Trp Gln Pro His Ser Lys Gln Asp Asp Met Trp Glu His Ile
 465 470 475 480

173/175

Ala	Thr	Phe	Asn	Ala	Leu	Gly	Tyr	Val	Gln	Ala	Ser	Lys	Arg	Asp	Lys
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Lys	Phe	Phe	Ala	Cys	Ala	Pro	Asn	Tyr	Ser	Tyr	Ala	Ala	Leu	Cys	Glu
		500					505						510		
Cys	Leu	Arg	Arg	Val	Phe	Ile	Tyr	Arg	Gln	Pro	Ala	Pro	Met	Ser	Thr
		515				520					525				
Val	Leu	Tyr	Asn	Arg	Lys	Glu	Gly	Arg	Gln	Val	Gly	Gln	Val	Ala	Lys
	530					535					540				
Gln	Gln	Val	Ala	Ser	Leu	Glu	Thr	Asn	Asp	Pro	Ile	Leu	Gly	Phe	Gln
545					550				555						560
Ala	Thr	Asn	Glu	Arg	Leu	Phe	Val	Leu	Thr	Thr	Lys	Asn	Leu	Phe	Leu
			565					570					575		
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			580												

<210> 150

<211> 30

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 150

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30

<210> 151

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 151

gaggctgaag acggcctatg tggccttttt tttttttttt tt

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<210> 152

<211> 21

<212> DNA

<213> Artificial Sequence

<220>



174/175

<223> Description of Artificial Sequence: artificially
synthesized sequence

<400> 152

agcatcgagt cggccttggt g

21

<210> 153

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially
synthesized sequence

<400> 153

gcggctgaag acggcctatg t

21

<210> 154

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially
synthesized sequence

<400> 154

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20

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially
synthesized sequence

<400> 155

tgtgggaggt tttttctcta

20

<210> 156

<211> 17



2

3

4

5

175/175

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 156

gttttcccag tcacgac

17

<210> 157

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 157

caggaaacag ctatgac

17



INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/05063

A. CLASSIFICATION OF SUBJECT MATTER

Int.Cl⁷ C12N 15/12, C07K 14/47, C12N 5/10, C12N 1/21, C12N 1/19, C12P 21/02, C07K 16/18, G01N 33/53, G01N 33/577, C12Q 1/02, C12Q 1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int.Cl⁷ C12N 15/12, C07K 14/47, C12N 5/10, C12N 1/21, C12N 1/19, C12P 21/02, C07K 16/18, G01N 33/53, G01N 33/577, C12Q 1/02, C12Q 1/68

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

GenBank/EMBL/DDBJ/GeneSeq, SwissProt/PIR/GeneSeq, MEDLINE (STN)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO, 98/37094, A2 (GENETICS INST. INC.), 27 August, 1998 (27.08.98) & AU, 9863373, A & EP, 971950, A2	1-13
P, X	WO, 99/55858, A2 (METAGEN GES. GENOMFORSCHUNG MBH), 04 November, 1999 (04.11.99) & DE, 19820190, A1	1-13
P, X	SUZUKI Y. et al., "Statistical analysis of the 5' untranslated region of human mRNA using "Oligo-Capped" cDNA libraries", Genomics (March 2000) Vol.64, No.3, pp.286-297	1-13

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:
 "A" document defining the general state of the art which is not considered to be of particular relevance
 "E" earlier document but published on or after the international filing date
 "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
 "O" document referring to an oral disclosure, use, exhibition or other means
 "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
 "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
 "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
 "&" document member of the same patent family

Date of the actual completion of the international search
19 October, 2000 (19.10.00)

Date of mailing of the international search report
31 October, 2000 (31.10.00)

Name and mailing address of the ISA/
Japanese Patent Office

Authorized officer

Facsimile No.

Telephone No.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/05063

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

The inventions as set forth in claims 1 to 13 are classified into 75 groups of inventions, i.e., inventions relating to DNA containing the base sequences represented in SEQ ID NOS : 1, 3, 5, 7, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 130, 132, 134, 136, 138, 140, 142, 144, 146 and 148 (each corresponding to a part of claims 1 to 13) and these groups of inventions are not considered as relating to a group of inventions so linked as to form a single general inventive concept.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Inventions relating to DNA containing the base sequence represented by SEQ ID NO:1 as set forth in claims 1 to 13.

- Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

A. 発明の属する分野の分類 (国際特許分類 (IPC))

Int. Cl⁷ C12N 15/12, C07K 14/47, C12N 5/10, C12N 1/21, C12N 1/19, C12P 21/02, C07K 16/18, G01N 33/53, G01N 33/577, C12Q 1/02, C12Q 1/68

B. 調査を行った分野

調査を行った最小限資料 (国際特許分類 (IPC))

Int. Cl⁷ C12N 15/12, C07K 14/47, C12N 5/10, C12N 1/21, C12N 1/19, C12P 21/02, C07K 16/18, G01N 33/53, G01N 33/577, C12Q 1/02, C12Q 1/68

最小限資料以外の資料で調査を行った分野に含まれるもの

国際調査で使用した電子データベース (データベースの名称、調査に使用した用語)

GenBank/EMBL/DBJ/GeneSeq, SwissProt/PIR/GeneSeq, MEDLINE (STN)

C. 関連すると認められる文献

引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
X	WO, 98/37094, A2 (GENETICS INST. INC.) 27. 8月. 1998 (27. 08. 98) & AU, 9863373, A & EP, 971950, A2	1-13
P, X	WO, 99/55858, A2 (METAGEN GES. GENOMFORSCHUNG MBH) 4. 11月. 1999 (04. 11. 99) & DE, 19820190, A1	1-13
P, X	SUZUKI, Y. et al. "Statistical analysis of the 5' untranslated region of human mRNA using "Oligo-Capped" cDNA libraries", Genomics (2000. Mar.) Vol. 64, No. 3, p. 286-297	1-13

☐ C欄の続きにも文献が列挙されている。

☐ パテントファミリーに関する別紙を参照。

* 引用文献のカテゴリー

「A」 特に関連のある文献ではなく、一般的技術水準を示すもの
「E」 国際出願日前の出願または特許であるが、国際出願日以後に公表されたもの
「L」 優先権主張に疑義を提起する文献又は他の文献の発行日若しくは他の特別な理由を確立するために引用する文献 (理由を付す)
「O」 口頭による開示、使用、展示等に言及する文献
「P」 国際出願日前で、かつ優先権の主張の基礎となる出願

の日の後に公表された文献

「T」 国際出願日又は優先日後に公表された文献であって出願と矛盾するものではなく、発明の原理又は理論の理解のために引用するもの
「X」 特に関連のある文献であって、当該文献のみで発明の新規性又は進歩性がないと考えられるもの
「Y」 特に関連のある文献であって、当該文献と他の1以上の文献との、当業者にとって自明である組合せによって進歩性がないと考えられるもの
「&」 同一パテントファミリー文献

国際調査を完了した日

19. 10. 00

国際調査報告の発送日

31.10.00

国際調査機関の名称及びあて先

日本国特許庁 (ISA/JP)

郵便番号 100-8915

東京都千代田区霞が関三丁目4番3号

特許庁審査官 (権限のある職員)

高堀 栄二

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電話番号 03-3581-1101 内線 3448

第Ⅰ欄 請求の範囲の一部の調査ができないときの意見 (第1ページの2の続き)

法第8条第3項(PCT17条(2)(a))の規定により、この国際調査報告は次の理由により請求の範囲の一部について作成しなかった。

1. ☐ 請求の範囲 _____ は、この国際調査機関が調査をすることを要しない対象に係るものである。つまり、
2. ☐ 請求の範囲 _____ は、有意義な国際調査をすることができる程度まで所定の要件を満たしていない国際出願の部分に係るものである。つまり、
3. ☐ 請求の範囲 _____ は、従属請求の範囲であってPCT規則6.4(a)の第2文及び第3文の規定に従って記載されていない。

第Ⅱ欄 発明の単一性が欠如しているときの意見 (第1ページの3の続き)

次に述べるようにこの国際出願に二以上の発明があるとこの国際調査機関は認めた。

請求の範囲1-13に記載された発明は、配列番号1、3、5、7、8、10、12、14、16、18、20、22、24、26、28、30、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、71、73、75、77、79、81、83、85、87、89、91、93、95、97、99、101、103、105、107、109、111、113、115、117、119、121、123、125、127、129、130、132、134、136、138、140、142、144、146、148に記載の塩基配列を含むDNAに係る発明群(それぞれ請求の範囲1-13の一部)の75の発明群に区分され、当該発明群が単一の一般的発明概念を形成するように連関している一群の発明であるとは認められない。

1. ☐ 出願人が必要な追加調査手数料をすべて期間内に納付したので、この国際調査報告は、すべての調査可能な請求の範囲について作成した。
2. ☐ 追加調査手数料を要求するまでもなく、すべての調査可能な請求の範囲について調査することができたので、追加調査手数料の納付を求めなかった。
3. ☐ 出願人が必要な追加調査手数料を一部のみしか期間内に納付しなかったため、この国際調査報告は、手数料の納付のあった次の請求の範囲のみについて作成した。
4. ☒ 出願人が必要な追加調査手数料を期間内に納付しなかったため、この国際調査報告は、請求の範囲の最初に記載されている発明に係る次の請求の範囲について作成した。

請求の範囲1-13の配列番号1に記載の塩基配列を含むDNAに係る発明

追加調査手数料の異議の申立てに関する注意

- ☐ 追加調査手数料の納付と共に出願人から異議申立てがあった。
- ☐ 追加調査手数料の納付と共に出願人から異議申立てがなかった。